

Best Local Similarity 99.8%; Pred. No. 3e-77;
Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 28 taaataaacactcatctatctatgattagataataataataatgcatcacactataaag 87
    |||||||
Db 1 TAAATATTAACACTTCTATTCATGATGATTAATATATATATGACATCATATATAG 60

Oy 88 taaacactctatcttcccccctcctcctcctcctcctcctcctcctcctcctcctc 147
    |||||||
Db 61 TAAACACTCTCATTTCTCCCTCCCTCTCATTTTATTACACACTTATATATTAAGTAC 120

Oy 148 tataagcatcacaccgttctgctactgatatcataaagtgttataatataataacta 207
    |||||||
Db 121 TATAGGATCATACACCGTTCGTTACTCGATCATATAAGTATTATTAATTAATACTA 180

Oy 208 tagatgcataaactcctacagatagatgcaataatcgtgttataaagaagaacatc 267
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Db 181 TAGATGCATTAATCTCATACAGAGTATGCATATCATTTGTTATTAAGAACACCATC 240

Oy 268 taaagctctctcctcgcagaccactctccctctgacaattgtagaagaactgcgacag 327
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Db 241 TAAACTCTTCTCCCTCCCGACGCTCCCTCTGACAAATTTAGAAAACTCGGCGCACG 300

Oy 328 ggaagcgccgaagttagatctcagcaactcgcgaagtgtgaagtctgcgcccact 387
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Db 301 GGAAGCGCGAGATGTAGATCTCAGCAAACTCGCAGTGTGAAGTCTGGCGCACCT 360

Oy 368 ggtgcatcacactgtttgctgcgaagctgtcgaacaataataaacaagacagatgaalt 447
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Db 361 GGTGATACACTGTGTGCTGCGCAAGCTGTGAAACAATATTAACACGACAGATGAAT 420

Oy 448 cctgcagtggaagcttggaattctgtaacacacatctcattgcgcaagtggttcagtt 507
    |||||||
Db 421 CCTGAGTGGGAGCTTGATTTTCGTAAACACACAACTCATTTGCCAAGTTGTTCCAGTT 480

Oy 508 gtagcagagatacagtcacacacacatgagagatactc 545
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Db 481 GCAGCAGGATATCATGTCACCAACCAATGAGATATTC 518

RESULT 2
AV562377 494 bp mRNA linear EST 07-SEP-2000
LOCUS AV562377 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone S0169b07F 3', mRNA sequence.
ACCESSION AV562377
VERSION AV562377.1 GI:8733803
KEYWORDS EST.
SOURCE
ORGANISM Arabidopsis thaliana
            thale cress.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 494)
REFERENCE
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
SOURCE
1. 494
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="S0169b07F"
/clone_1lb="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 155 a 113 c 81 g 145 t
ORIGIN

Query Match 57.7%; Score 494; DB 9; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 29 aaataaacactcatctatctatgattagataataataataatgcatcacactataaagt 88
    |||||||
Db 1 AAATATTAACACTTCTATTCATGATGATTAATATATATATGACATCATATTAAGT 60

Oy 89 aaaaacactctcatcttcccccctcctcctcctcctcctcctcctcctcctcctcct 148
    |||||||
Db 61 AAAACACTCTCATTTTCCCTCCCTCTCATTTTATTACACACTTATTAAGTACTACT 120

Oy 149 ataggcatcacaccgttctgctactgatatcataaagtgttataatataataactat 208
    |||||||
Db 121 ATAGGATCATCACCGTTCGTTACTCGATCATATAAAGTATTATTAATTAATACATAT 180

Oy 209 agatgcataaactcctacagatagatgcaataatcgtgttataaagaagaagccact 268
    |||||||
Db 181 AGATGCATTAATCTCATACAGAGTATGCATATCATTTGTTATTAAGAACAGCATCT 240

Oy 269 aaagctctctcctcgcagaccactctccctctgacaaltgtagaagaactgcgacag 328
    |||||||
Db 241 AAAGTCTTCTCTCCCGACGACCTCCCTCTGACAAATTTGTAAGAACTGGCGCACG 300

Oy 329 gaaagcggaagattgtagatctcagcaactcgcgaagtgttgaagtctgcgcccactg 388
    |||||||
Db 301 GAAAGCGGAGATTTGATGATCTCAGCAAACTCGCAGTGTGAAGTCTGGCGCACCTG 360

Oy 389 gtcatacacactgttgcctgcgaagctgtcgaacaataataaacaagacagatgaaltc 448
    |||||||
Db 361 GTGATACACTGTTTGCTGCGCAACCTGTGCAAAATATTAACGACAGATGAATTC 420

Oy 449 ctgcagtggaagcttggaattctgtaacacacatctcattgcgcaagtggttcagttg 508
    |||||||
Db 421 CTGCAGTGGGAGCTTGATTTTCGTAAACACACAACTCATTTGCCAAGTGTTCAGTTG 480

Oy 509 tagcagagatacga 522
    |||||||
Db 481 TAGCAGGATATCA 494

RESULT 3
BE590867/c 551 bp mRNA linear EST 18-AUG-2000
LOCUS BE590867 WHE0855_C01_E012S wheat 20-45 DAP spike cDNA library Trilicium
DEFINITION aestivum cDNA clone WHE0855_C01_E01, mRNA sequence.
ACCESSION BE590867
VERSION BE590867.1 GI:9845940
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Triticum.
            1 (bases 1 to 551)
REFERENCE
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes - 20-45 DAP spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
```


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Tel: 5105595773
Fax: 5105595818

Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES

source 1..505
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0963_B10_C19"
/clone.lib="Wheat pre-anthesis spike cDNA library"
/tissue.type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli S01R"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site.1: EcoRI; Site.2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plusescript phagemids in the Tj Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 99 a 148 c 160 g 98 t
ORIGIN

Query Match 23.2%; Score 198.4; DB 10; Length 505;
Best Local Similarity 67.3%; Pred. No. 5.3e-24;
Matches 280; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
QY 364 ggtgtgaattcttggtgacacccctggtgacatacctggtgacacacgctggaac 423
DB 504 ggtgtgaattcttggtgacacccctggtgacacacgctggaac 445
QY 424 aatataacacgacacgacgaattctcgtgacgtggaattctgtaacacacac 483
DB 444 agtagcagacacacgacggtgacgtgacgtgacgtgacgtgacgtgacgtgac 385
QY 484 tcaatgacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 543
DB 384 tctctgacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 325
QY 544 tctctgacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 603
DB 324 tccctgaagcttggtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 265
QY 604 aagttctgacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 663
DB 264 aagttctgacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 205
QY 664 cttaagatcaacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 723
DB 204 ttgagctgacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 145
QY 724 cttaagatcaacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 779
DB 144 cggagacacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 89

RESULT 6
BF483056 491 bp mRNA linear EST 06-DEC-2000
LOCUS WHE2314_C03_E06ZS wheat pre-anthesis spike cDNA library Triticum
DEFINITION WHE2314_C03_E06ZS wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE2314_C03_E06, mRNA sequence.
ACCESSION BF483056
VERSION BF483056.1 GI:11566357

KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
NCBI Taxonomy Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Pooidae
; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 491)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Iazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES

source 1..491
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2314_C03_E06"
/clone.lib="Wheat pre-anthesis spike cDNA library"
/tissue.type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli S01R"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site.1: EcoRI; Site.2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plusescript phagemids in the Tj Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 93 a 145 c 151 g 101 t 1 others
ORIGIN

Query Match 23.0%; Score 196.8; DB 10; Length 491;
Best Local Similarity 67.5%; Pred. No. 9.9e-24;
Matches 276; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 371 agttctgacacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 430
DB 491 agttctgacacacacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 432
QY 431 acacgac 490
DB 431 acacgac 372
QY 491 caaaggttgcac 550
DB 371 ncaagac 312
QY 551 ggtgaggttctgtagacttggaac 610
DB 311 ggtgaggttctgtagacttggaac 252
QY 611 tgaggttcttccac 670
DB 251 tcattcattgac 192
QY 671 ccaagcattgac 730

Db	191	CGCAGCCTTGGACACGGTCTCCTGTTCCAGAAAGAAACCTGAGTTGGTGGTCCGGATGA	132
Oy	731	acggatcaagaagctctccaaactcgtctactataagaaggtctct	779
Db	131	AGGGGTCCAGCAGCTCCGCCCAACCCCTGCAACACCACGCGGGTCTCT	83
RESULT	7		
LOCUS	AV937451/c	542 bp	linear
DEFINITION	AV937451 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves	Hordeum vulgare subsp. spontaneum	EST 18-JAN-2002
ACCESSION	AV937451		
VERSION	AV937451.1	GI:18233248	
KEYWORDS	EST.		
SOURCE	Hordeum vulgare subsp. spontaneum.		
ORGANISM	Hordeum vulgare subsp. spontaneum		
REFERENCE	Eukaryote, Viridiplantae, Streptotum		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae		
TITLE	1 (bases 1 to 542)		
JOURNAL	Sato, K., Saisho, D. and Takeda, K.		
COMMENT	Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002) Contact: Tadasu Shln-i Center For Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshln@genes.nig.ac.jp. Location/Qualifiers 1..542		
FEATURES	source		
	/organism="Hordeum vulgare subsp. spontaneum"		
	/strain="H602"		
	/db_xref="taxon:77009"		
	/clone_id="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"		
	/issue_type="top three leaves"		
	/dev_stage="adult, heading stage"		
BASE COUNT	120 a 150 c 146 g 124 t	2 others	
ORIGIN			
Query Match	21.6%: Score 184.6; DB 9; Length 542;		
Best Local Similarity	62.6%: Pred. No. 1.1e-21;		
Matches	303; Conservative 0; Mismatches 180; Indels 1; Gaps 1;		
Oy	274	ctctctccgcgcagcacactctccctctgaacaattgtlaaanaactcgcgcagcggaaag	333
Db	502	CTCCTCCCGCGGTCGCCGTGGAGCGTGGAGTTGAAGTTACACGGCGCGCGCTTG	443
Oy	334	ccgagatgtatgaltctcagcaaaactcgcagtglttgaagtctcgcgcaccctgtgtca	393
Db	442	CCAAAGTTGAAGCGCGCGCGAGAGCTGCGTAGTGAAGCTCTGGCGGCTGTGGCCG	383
Oy	394	tacactgtttgctgcgcgaagctgtgtgaacaatataaacagacacgcagatgattctga	453
Db	382	AACACCGTCCCGCCCGCCAGCTGCTGTACAGAACCATATACCATGCGGTGGATGCCATA	323
Oy	454	gtggactgtgattctcgtlaaacacaacaatctcatctgcacaaagtgttcagttgagca	513
Db	322	GTAAGGTTTGGGCTCTGATATGCGACGANTCTTTTCCAAAGCTATCGTTTGTTATGCT	263
Oy	514	gggatatagtcacaacaaatgagatatcttcggaagtgaaggttctagactgtga	573
Db	262	GGGACATCATGACCATCATGACGTGACGATACGCCCAAGGTTGGGTTGCTGGATTAGGC	203
Oy	574	acatctgtatcacaataccaagaatagaaagttcctcgaggtctcttcacaacattcca	633
Db	202	GCANAGGATCCACCATACTAGAGTTATATAGGCAACAGAAATCATCATCAACATCTCA	143

QY	634	acccttgctgtttttagaagcgcgaagaagcccttagatccaagccatttagtaacctctctt	693
Db	142	ACGGTGGGTTTCAGAGCATCTGCTGTTAGTGAGCAAACTCCATTCCTTAACAACAGGCTTC	83
QY	694	tggccataagtaaccttagagtgatgtatctatctaaac-cgatcaagaacgtctccaac	752
Db	82	CCATCATCATCTACAGCTTAGAGGCACTGACGTAAACAATGGTTTCTAGAACATCTCCAAC	23
QY	753	aact	756
Db	22	TAT	19
RESULT	8		
LOCUS	B6647258/c	781 bp	linear
DEFINITION	EST508867 HOGA Medicago truncatula cDNA clone pHOGA-1619 5' end,		
ACCESSION	B6647258		
VERSION	B6647258.1	GI:13782360	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Hahn,M.G., Ojansen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,		
UTTERBACK,T., Cho,J. and Fraser,C.M.			
ESTs from roots of Medicago truncatula treated with			
oligolacturonides of Dp 6-20			
unpublished (2001)			
JOURNAL	Contract: Michael G. Hahn		
COMMENT	Complex Carbohydrate Research Center		
	University of Georgia		
	220 Riverbend Road, Athens, GA 30602-4712, USA		
	Tel: 706-542-4457		
	Fax: 706-542-4412		
	Email: hahn@ccrc.uga.edu		
	G350854e TIGR sequence name: MTMBW537K More information is		
	available at: www.medicago.org		
	Seq primer: SKmod (CTA gaa cta gta gat cc).		
FEATURES	Location/Qualifiers		
Source	1. 781		
	/organism="Medicago truncatula"		
	/cultivar="A17"		
	/db_xref="taxon:3880"		
	/clone="pHOGA-1619"		
	/clone.lib="HOGA"		
	/tissue.type="3 day old seedling roots"		
	/dex.stages="24 hours after treatment in the dark at 26 C		
	with 0.5 mg/ml oligogalacturonides (dp 6-20) in the		
	presence of 100 ug/ml Gentamicin"		
	/lab.host="XLOLR"		
	/note="Vector: pBluescript SK-. Site.1: EcoRI; Site.2:		
	XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA		
	was directionally ligated into the unizap XR vector from		
	Stratagene and packaged using GigaPack III Gold packaging		
	extracts. Plasmids containing cDNA inserts were excised		
	from the recombinant lambda-Zap phage using Ex-assist		
	helper phage and propagated in SOUR cells."		
BASE COUNT	243 a	147 c	150 g
ORIGIN	241 t		
Query Match	21.1%;	Score 181;	DB 10; Length 781;
Best Local Similarity	59.4%;	Pred. No. 3.7e-21;	
Matches	326;	Conservative 0;	Mismatches 220; Indels 3; Gaps 1;
QY	251	taagaagaagcactctaaagctctctcttcgcgcgacactctccctctgacaattgtc	310

Db	605	TATAGTGTCTATGAGTATGTACTAGCGCTTCTTGACAGCGGTTTCTCTGACATTGA	546
Qy	311	agaaacatctgcygcaacggaagccgagattgttagatctcagcaaacctcgagtggttga	370
Db	545	AGTAATACGACGACCAACAGGAGACCCAGATCATCTCTGTGACAAATATGCAAGTGTGA	486
Qy	371	agttctgagcccaacctgg---tgatcacactgttgcctgcgaagctgctgaaacaata	427
Db	485	AGTAATCCCTTGAGATGGTATGCTGTACATGATTTCTTATTTCTTGTTCATATAGAA	426
Qy	428	taaacacgacacgaatgaattccctcagtgagtgagacttgatlltcgtaaacacacatctcat	487
Db	425	CAAAACACAACCTGTGTATACCTATATTTGGCTTTGGTATCTCATAGCTCACTACTTCTT	366
Qy	488	tgccaaaggttgttccaglttgtagcaggagatalcagtcaccacaaatgagagatalctc	547
Db	365	TCCCAAAAGTACATCTGTGTTCCAGGAAATATCTGTGCATTCACAGTGCAGATGTATC	306
Qy	548	ggaagtgagggtgtcgttagagacttggaaacatctcgatccacacataacaaagtatagaagt	607
Db	305	TTAGATTAAGGATCACTAGAGGCCGAGGAACATTCAGGGCTGTCTATCAACAGTATATGAAG	246
Qy	608	tccttaggtctcttcacacacatctcaactcttgagcttgtttgaaacctgagaagcccta	667
Db	245	ACCTCATGTCTACCCACCATCATATCTTAACCTTTGGGTTTGCTTGTGATAGTGGAGGAGAA	186
Qy	668	gatccaagacatltagtcacactcctctcttgccataagtaaacctttagagtatgatalcat	727
Db	185	ACTCATGGCGCATTTGAAGACTTCTCTTGTGTGTACTCATCATATTTTCATGCTGTGTGG	126
Qy	728	taaacggatcaaagaacgtctccacaacactctgcttactataagagagctcttataatta	787
Db	125	TAAAGATTCAGAAAGACTTCTCTATCATCTTCCAAACATGATGATGTCTTGAGACATTC	66
Qy	788	tagacatct 796	
Db	65	TTGCGCATTT 57	
RESULT	9		
LOCUS	BM407295/c	718 bp	linear
DEFINITION	EST581622 potato roots Solanum tuberosum cDNA clone CPRO30M16 5'		EST 22-JAN-2003
ACCESSION	BM407295		
VERSION	BM407295.1		
KEYWORDS	EST.		
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Empirypophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
AUTHORS	1 (bases 1 to 718) van der Hoeven, R., Sun, H., Karawycheva, S.A., Tsai, J., Van Aken, S., Utecherack, T., Chieningo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksey, S. and Baker, B.		
TITLE	Generation of ESTs from potato roots		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195 Email: cdna@resgen.com For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: T3.		

```

/lab host="SOLR"
/note="vector: bluescript SK(-): Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University, Tankley lab;
sequencing: The institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
BASE COUNT      243 a      128 c      142 g      205 t
ORIGIN

```

Query Match	20.2%	Score 173.2	DB 10	Length 718
Best Local Similarity	60.2%	Pred. No. 7.7e-20		
Matches 324	Conservative 0	Mismatches 208	Indels 6	Gaps 2
Oy	273	tcctctccctccgcagccactctccctctgcaaatgtgagaacctgcygcacgggaag	332	
Db	565	tcactcttcttgcagcagcgtttcttcttggcatttaagtgagcagcagcaacaggga	506	
Oy	333	gccgagattgtgatactcagcaactgcgagtggttgaaagttctgycgccaccctggtgc	392	
Db	505	accgaatccattttctgcgcgcaaaattttgaaatggtgaatgatctcttggtaacgtga	446	
Oy	393	atacactgttgcctgcgc---aagctgtgcgaacaataaacaacagcagcgaatgcc	449	
Db	445	tttctactgtttttcttcccttatttttgcccttattatagaaacagctatcgatgaatccc	386	
Oy	450	tgcagtggaacttggatlltcgtaacacacaatcctcatctgccaagaagtgtccagttgt	509	
Db	385	gattcactggttttgagactatcgtactgctacttcttccaaaagaagcactgattga	326	
Oy	510	agcagggatatactgcacccaacttggatataatctcggaggttgaaggttctatggact	569	
Db	335	accagagaattatctgcacaaatccactgaggggttcccttaagtaaggctactgagac	266	
Oy	570	tggaaactctgtgataccacataaccaagaatagaaagttccctgaggtcttcccaacat	629	
Db	265	tggaaacatcttgatctagatcatgatgatgatgatgatgatgatgatgatgatgatgat	206	
Oy	630	ctcaactcttggctgtgttlltgaaacttgaagagccttgaatccaaagccatagtaacctc	689	
Db	205	ctccacacagagccttgaagaacatgatagagagcctgtaactgataccatttaaaccttg	146	
Oy	650	t---cttggccataagaactcttaaggttgatctatataaaccgataaagaagctc	746	
Db	145	tttggcttcattattattatcacaattatatttttccacttggattggaactttacactgacttc	86	
Oy	747	tccaaacaactctgctactaataaagggtctcttatattatagacatcttggacttt	804	
Db	85	tccatttcaactcttggacaacatattggttcttcaattatcttacaagaacattttatccctt	28	
RESULT 10				
BH558079/c		395 bp	DNA	Linear
LOCUS	BH558079			GSS 14-DEC-2001
DEFINITION	BOGFM69T BOGF Brassica oleracea genomic clone BOGFM69, DNA			
ACCESSION	BH558079			
VERSION	BH558079.1			
KEYWORDS	GSS.			
SOURCE	Brassica oleracea.			
ORGANISM	Brassica oleracea			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			

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Location/Qualifiers
1. 718
/organism="Solanium tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPR030M16"
/clone_lib="potato_roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
```

REFERENCE 1 (bases 1 to 395)
AUTHORS Town, C.D., Van Aken, S., Uteirack, T. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of *Brassica oleracea*
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BCGFM69TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523
Fax: 301-838-0208
Email: cdhowett@tr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source
Location/Qualifiers

1..395
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGFM69"
/clone_1ib="BOGF"
/note="Vector: PHOS1; Site.1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 107 a 81 c 85 g 122 t
ORIGIN

Query Match 17.6%; Score 150.8; DB 12; Length 395;
Best local Similarity 80.7%; Pred. No. 5.4e-16;
Matches 176; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 274 cttctctcgcgagcactctccttgacaattgtagaanaactgcgacggaag 333
|||||
Db 386 CTCTCTCTCCGACGACATCTCTCACTGACAGTGAACAGACGACGACGAGGAGA 327

Qy 334 ccgaagtttagatctcagaanaactgcgaggtgtgaagtctggtgcccactgtgca 393
|||||
Db 326 CCAGAGTTTGAATGACGAGAACTCAGCGAGTGTGAACCTTGCCGCTAGAGGCA 267

Qy 394 tacaactgttcctcgaactgtcgaanaactgaacacagacagatgaattcctgca 453
|||||
Db 266 TAAACAGTTTGTCTTCGAGATTTCGGAACATATCATCATCGACTCGGTGATTTGAA 207

Qy 454 gtggactgtgatttcgttaacacacatcgaatgcc 491
|||||
Db 206 GTGGAGATGATGATTCGTGATACACCACTCATTTGCC 169

RESULT 11
BE602964/c 520 bp mRNA linear EST 22-OCT-2001
LOCUS HVSMEH010D16f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HVCNNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH010D16f,
mRNA sequence.
ACCESSION BE602964
VERSION BE602964.3 GI:16322734
KEYWORDS EST.
SOURCE
ORGANISM Hordeum vulgare
barley.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 520)
Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton
, R. D., Close, S. J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:13190740.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 405
Seq primer: AATTACCTCTCACTAAGG
High quality sequence stop: 513.
Location/Qualifiers

source

1..520
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH010D16f"
/clone_1ib="Hordeum vulgare 5-45 DAP spike EST library
HVCNNA0009 (5 to 45 DAP)"
/issue_type="5-45 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million plv were
in vivo excised to give phagescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)"

BASE COUNT 84 a 108 c 184 g 84 t
ORIGIN

Query Match 17.1%; Score 146.8; DB 10; Length 520;
Best local Similarity 60.6%; Pred. No. 2.3e-15;
Matches 241; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 381 ccaacctggtgcatcactgtttgctcgaactgtcgaanaactaataacacgacag 440
|||||

Db 520 CCACCCCGGGGCGTACACCGTGTGCGCGAGTGTGGAAGACGAAACACACTCG 461

Qy 441 atgaattcctgcagtggaatttgcgttaacacacatcattccaaagtgt 500
|||||

Db 460 GTGGATCCGAGCACCGCGCGCCCTCTGTACACACCAACCTCGGTACCAAGACAC 401

Qy 501 tccagttgtagcagggatcagtcacacacacatgaagatattctcgaggtgaggt 560
|||||

Db 400 TCTGTGTGCGCGGAGTGTGCGTACACGCAAGTACTCTTAAGGCTGGGCTC 341

Qy 561 gctagagacttgaacatctgataccacacacacacacacacacacacacacac 620
|||||

Db 340 GCTGGGCTTGGAGCATCCGATCCACATCACCAGGCTGAAGAGTGGCATGTCCG 281

Qy 621 tccacacatcacaactgtgtgtttgaacctggaagacccatgatacgaacatt 680
|||||

Db 280 GCCGCCGACCTCGACGCGCGGTGTGCGGAGTGGCGGAGCGCGAGCTCGCAGCGCTT 221

Qy 681 agtcaactctcttggacataagtaaccttaagatgattatcattaaagatgaag 740
|||||

Db 220 GGCCAGCTCCCTGAGCGGAGCGGACCGGACCGGCGGACGAGAGGGGTCCAC 161

Qy 741 aacgtctcaacaacactgtcttactataaagaggtctc 778
|||||

Db 160 CACGTGCGCATCATCCGCGCCACACACACGAGGCTCC 123

FEATURES

RESULT 12
BF259482/c

LOCUS BF259482 574 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSMEF0019D18f Hordeum vulgare seedling root EST library HVCNDA0007
 (Elicited and unstressed) Hordeum vulgare cDNA clone
 HVSMEF0019D18f, mRNA sequence.
 ACCSSION BF259482
 VERSION BF259482.2 GI:13119945
 SOURCE EST.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 574)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
 , R.D., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex unstressed seedling root cDNA library
 Unpublished (2001)
 On Nov 16, 2000 this sequence version replaced gi:11188511.
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 426
 Seq primer: AATTACCTCCTCCTAAGG
 High quality sequence stop: 572.
 FEATURES
 source
 1. 574
 Location/Qualifiers
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEF0019D18f"
 /clone_lib="Hordeum vulgare seedling root EST library
 HVCNDA0007 (Elicited and unstressed)"
 /tissue_type="Seedling root"
 /lab_host="TVC121"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under aseptic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedling roots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pfu were in vivo excised to give plasmid
 SK(-) cDNA phagemids. These steps were performed in the TU
 Close laboratory at the University of California,
 Riverside (Choi, Close, Fenton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

BASE COUNT 150 a 141 c 131 g 152 t
 ORIGIN
 Query Match 16.7%; Score 143; DB 10; Length 574;
 Best Local Similarity 60.4%; Pred. No. 9.5e-15;
 Matches 236; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Oy 290 cactctcccttcgaacatgtagaacactgcgcgaaggagccgagatctagatct 349
 || ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 396 CAGTCTCTCTGACAGTAAATACAGCTGCCACCTGGAGGCCGCGAGTCATTCTCT 337
 Oy 350 cagcaactcgcgagtggttagatcttcggccaccctcgfgcgactacacttgcctgc 409
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 336 CAGCAAACTGACGGGTGTGAACGTGATCTGAAAGAAAGACAGTTACAGCTGCTTC 277
 Oy 410 caagctgcgaacaatataacacgacacgacgataatctcgcagtggaattgatct 469
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 276 GCTTCTGCTTAAAGACGCAAAAATGAAACCTGTGATGCTTGGGCTTGGGCTCT 217
 Oy 470 cytaacacacacatcattcgcacaaagtggttcagatgttagcaggaatcagtacca 529
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 216 CATGCTTATACCTCCCGCTCAAAAGAACATCTGTTGCCAGTATATACAGTACAA 157
 Oy 530 accaatgagatattctcggagtgagtggtgcgcagactgcacatcgcacacca 589
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 156 TCCAGTGAAGGTGCTCCTTGAATATGATGATCTTGCTTGCACATCAGGCTCTGCA 97
 Oy 590 taaccaagtagaagttcctcgtggtctctccacacacatcctcattgctgttt 649
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 96 TAACCACTGACACAGAGATGCGAGGCCATCCCTTGAGCCTTACTGTGTAGATA 37
 Oy 650 gaacctggaagcccttagatccaagccatt 680
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 36 CAACCGCTGATGGGTAGAGCTCATGGCCATT 6

RESULT 13
 BH542868/c 773 bp DNA linear GSS 14-DEC-2001
 LOCUS BOGJN29TF BOGJ Brassica oleracea genomic clone BOGJN29, DNA
 DEFINITION
 sequence.
 ACCSSION BH542868
 VERSION BH542868.1 GI:17794649
 KEYWORDS GSS.
 SOURCE
 ORGANISM Brassica oleracea.
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eucosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 773)
 Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 JOURNAL Other GSSs: BOGJN29TF
 COMMENT Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 FEATURES
 source
 1. 773
 Location/Qualifiers
 /organism="Brassica oleracea"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOGJN29"
 /clone_lib="BOGJ"
 /clone_lib="BOGJ"
 /note="Vector: pHOSt; Site_1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOSt using BstXI linkers"

BASE COUNT 214 a 158 c 166 g 235 t
 ORIGIN
 Query Match 16.6%; Score 142.2; DB 12; Length 773;
 Best Local Similarity 76.7%; Pred. No. 1.2e-14;
 Matches 174; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Y	265	atttaagctctcttcctccgcagacactctccctctacaattgtagaanaatcgcgc	324
Y	265	atttaagctctcttcctccgcagacactctccctctacaattgtagaanaatcgcgc	324
Db	367	ATCTATGTTCTTCTTCCTCCCGAGCATTGTCCTCTACAGTTGAAGAAGGCGACCC	308
Y	325	acgggaagccgagattgtagatctcagcaactcgcagatgttgaattctcgcgcac	384
Db	307	ACGGGTATACCAAGATTTGTTGTTCTCAGCAAGACGACGAGTGTTCAGACGTTGGCGCAC	248
Y	385	ctcgtgtcatacaactgtttgcctgcgaacgctgtgcgaacaataataacagacagatga	444
Db	247	TCAGGTGATCAAAACCGTTTGCTCTCTGTGAGTTGCCGGGCAACAATCATGATGCTACTCGTGA	188
Y	445	attctctcagatggagactgattcttcgtaacaacacatcatctatgccc	491
Db	187	ATTCTGGAATTGGACATGGTTCTCATATGTCACCAATTCATTGTC	141
RESULT 14			
LOCUS	AL385107/c		
DEFINITION	AL385107	459 bp	MRNA
ACCESSION	AL385107		linear
VERSION	AL385107.1		EST 03-AUG-2000
KEYWORDS	GI:9684858		
SOURCE	EST.		
ORGANISM	barrel medic.		
	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
REFERENCE	1 (bases 1 to 459)		
AUTHORS	Journet,E.P., Crespeau,H., van Tuinen,D., Gouzy,J., Jallou,O., Nibbel,A., Carreau,V., Chataigner,O., Kahn,D., Glanmazzi-Pearson,V. and Gamas,P.		
TITLE	Medicago truncatula ESTs from endomycorrhizal roots		
JOURNAL	unpublished (2000)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Molculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-est@toulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html). Location/Qualifiers 1.459 /organism="Medicago truncatula" /cultivar="Jemalong" /db_xref="taxon:3880" /clone="MEBC26D07" /clone_lib="MEBC" /tissue_type="arbuscular mycorrhiza" /dev_stage="harvested 3 weeks post inoculation with Glomus intraradices" /note="Vector: pBluescript PSK. Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epioises soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using GigaPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExSait helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of		

BASE COUNT	150 a	88 c	91 g	130 t
ORIGIN	fungal origin."			
Query Match	16.5%; Score 141; DB 9; Length 459;			
Best Local Similarity	61.5%; Pred. No. 2.2e-14;			
Matches 244; Conservative 0; Mismatches 150; Indels 3; Gaps 1;				
OY 251	taaagaagaagccatctcaagctctctccgcgacgaactctccctctgacaattgt 310			
Db 397	TATAGTGCTATGGCTATGTAGCTAGCGCTTCTTGACAGCGGTTCTCTCGAGCATTTGA 338			
OY 311	agaagaatctgcggccagggaaagccgagatctgtagatctcagcaaacctcgagtggtga 370			
Db 337	AGTAACAGCAGCAACAGGAGACCAAGATCATTTCTGTGAAGCAAAATTTGGAGGTGTGA 278			
OY 371	agcttcggcgccacccctgg---tgcatcacagctctgcacgaactcgcaagctcgtaaacata 427			
Db 277	AGTAATCCCTTGAGATGTGTATGCTGTCACTGATTCCTATCTTTTGTGTTGAATAGAA 218			
OY 428	taaacacgacacgataatctccgtcagtcggagactgtgaatttcgttaacacaaactcat 487			
Db 217	CAACACCAACCTGTGTATACCTATATTTGGCTTTGGATGTCAATAGCTCACTACTTCTT 158			
OY 488	tgccaaagcttgctccagttgttagcaggagatacagtaaccaacatgagagatacttc 547			
Db 157	TCCCAAAATGTAGCANTCTTTGTTCCAGGAATATCTGTCAATCCAGTGCAGCAAGTGTCTC 98			
OY 548	ggaagtgagaggttgtagagacttgtaaacatctgtaattccacataaccaaagtatagaag 607			
Db 97	TTAGATTAAAGATCACTAGAGCCAGGAAACATCAGGGCTGTCTCATCCAGTGTATAGAAAG 38			
OY 608	tccctgaagctctctccaccaatctcaactctctgactt 644			
Db 37	ACCTCATGTGCAACCACTCAATCATCTTGCGTTT 1			
RESULT 15	BE319228 432 bp mRNA linear EST 20-DEC-2000			
LOCUS	NF015E08R1F1055 Developing root Medicago truncatula cDNA clone			
DEFINITION	NF015E08R1 5', mRNA sequence.			
ACCESSION	BE319228			
VERSION	BE319228..2 GI:11928492			
KEYWORDS	EST.			
SOURCE	barrel medic.			
ORGANISM	Medicago truncatula			
REFERENCE	EnxarVola, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Watson,B.S., Shih,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,			
TITLE	Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,D.T., Weller,D.W., May			
JOURNAL	Expressed Sequence Tags from the Samuel Roberts Noble Foundation			
COMMENT	Medicago truncatula root library			
FEATURES	Seq primer: TCACACAGGAACACGCTATGAC.			
source	Location/Qualifiers			
	I..432			

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/organism="Medicago truncatula"  
/db_xref="taxon:3880"  
/clone="NF015E08RT"  
/clone_lib="Developing root"  
/tissue_type="root"  
/dev_stage="pooled developmental"  
/note="Vector: Lambda Zap; Total RNA was extracted from  
non-nodulated roots of plants grown in 1 mM nitrate  
medium. Samples were taken at four time points  
(approximately two days, one, two and six weeks post  
germination) representing early seedling growth to  
nitrogen limitation."   
BASE COUNT      126 a      85 c      88 g      133 t  
ORIGIN
```

```
Query Match      16.4%; Score 140.8; DB 10; Length 432;  
Best Local Similarity 61.4%; Pred. No. 2.5e-14;  
Matches 226; Conservative 0; Mismatches 142; Indels 0; Gaps 0;  
  
QY 429 aaacagacagatgaatcctcgtcagtggaacttggaatttcgtaacacacaaatcatt 488  
    || || | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 426 AACACAAACCTGCTATACCTATATTGGCTTGGTATCTCATAGCTCATCTTCTTT 367  
  
QY 489 gccaaaggctgtccagttgtacagagataatcagtcaccaaccaatggagatatctcg 548  
    || || | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 366 CCCAATGTAGCATCTGTGTCCAGGAATATCTGCATCAATCCAGTGCACACTGTTCTCT 307  
  
QY 549 gaggtgagggtgtcgtgagacacttggaacatcgtaccacataaccataagatagaagt 608  
    || || | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 306 TAGATTAAGGATCATTAGGCCAGGAACATCAAGGTCTGTCAATCACCAGTATAGAAAGA 247  
  
QY 609 cctgaggtctctccaccaatcctcaactcttggtgtgttggaacctggaagagccttag 668  
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 246 CCTCATGTGCACCATCATCTCAACTTTGGGTTTGGTGTGATAGTGAAGGAAANA 187  
  
QY 669 atccaagcattagtcacctctctcttgccataaagtaacctttagagatgatctatt 728  
    || || || || || | | | | | | | | | | | | | | | | | | | | | |  
DB 186 CTCATGGCCATTGAAGACTTGTCTTGTGTACTCACAGTCATTTTCATGCTGTGGT 127  
  
QY 729 aaacgatacaagaagctctccacaacactcgtactataaagaggtctctatatattat 788  
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 126 AAAGAAATCAAGAACTTCTCTTATCCTCTTCCAAACAATGAGTGGTCTTGAGACATTCT 67  
  
QY 789 agaatct 796  
    | | | | |  
DB 66 TGCCATT 59
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Search completed: September 14, 2002, 18:25:04
Job time: 23469 sec

Db	361	cgagtggtgaagctctcggcgcaacctgggtgatacaactgtttgctctgcaagctgtlga	420
Oy	421	aacaatabaaacacgacacagatgaatctctgcagctggagacttggatttctgtaacacaa	480
Db	421	aacaatabaaacacgacacagatgaatctctgcagctggagacttggatttctgtaacacaa	480
Oy	481	atcccatgtcccaaggttgcttccagttgttagcaggagatatcagtaaccaacaatggagaa	540
Db	481	atcccatgtcccaaggttgcttccagttgttagcaggagatalcagtaaccaacaatggagaa	540
Oy	541	tatctccgaggtgaaggcttgcctaggaacttggaaactcggatccaccaataaccaagta	600
Db	541	tatctccgaggtgaaggcttgcctaggaacttggaaactcggatccaccaataaccaagta	600
Oy	601	tagaagttcctgaaggtctctctccaccaatctcaactcttgcttgtttttggaaactggaaa	660
Db	601	tagaagttcctgaaggtctctctccaccaatctcaactcttgcttgtttttggaaactggaaa	660
Oy	661	ggccttgatgccaaagcccatagtcactctctcttcttgccaataagtaacctttgaatgatt	720
Db	661	ggccttgatgccaaagcccatagtcactctctcttcttgccaataagtaacctttgaatgatt	720
Oy	721	gactatataaacggatacaagaacgtctccacaacactcgtactactaataagaggtccttt	780
Db	721	gactatataaacggatacaagaacgtctccacaacactcgtactactaataagaggtccttt	780
Oy	781	atatattatagacatcttgaatctctgaaacaacctcgttgctgaattctctcgaagcccgagg	840
Db	781	atatattatagacatcttgaatctctgaaacaacctcgttgctgaattctctcgaagcccgagg	840
Oy	841	atccactagttctaga	856
Db	841	atccactagttctaga	856
RESULT 2			
US-09-060-726a-1/c			
Sequence 1, Application US/09060726a			
Patent No. 6225530			
GENERAL INFORMATION:			
APPLICANT: Weigel, Detlef			
APPLICANT: Salk Institute			
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY			
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT			
FILE REFERENCE: SALKINS.026A			
CURRENT APPLICATION NUMBER: US/09/060,726A			
CURRENT FILING DATE: 1998-04-15			
NUMBER OF SEQ ID NOS: 13			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 1			
LENGTH: 855			
TYPE: DNA			
ORGANISM: Arabidopsis thaliana			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (63)...(590)			
US-09-060-726a-1			

	Query Match	Similarity	Score	DB 4.2	Length	855
	Best Local	85.4	99.8%	Pred. No. 3.3e-214		
	Matches	854	Conservative	0	Matches 1	Indels 1
Qy	1	ctcgaatttttttttttttttttttataaataaacaattcatctatgataaata	60			
Db	855	ctcgaatttttttttttttttttttataaataaacaattcatctatgataaata	796			
Qy	61	taattatcgatcacacaactatataagtaaaacactctatcttcccccctcat	120			
Db	795	taattatcgatcacacaactatataagtaaaacactctatcttcccccctcat	736			
Qy	121	ttattacaacttatatatatgaactactaaggaacacacagcttgcttactglatca	180			

Db	735	TTATTACACACTTATATTTGACTACTAGTATGGCATCATCAAGCTTGGTTACTCGTATCA	676
Qy	181	taaaatggtlataaataactatactatagatgcataaatccatccaglatatgcaat	240
Db	675	TAAATGGTTTATTAATTAAATTAATCTATAGATGCATTAATCTCATCGAGATATGCAATAT	616
Qy	241	caattgggtlataaagaagaagcaatctcaagttcttcttcctcgagccaaactctccctc	3000
Db	615	C-ATTGGTTATTAAGAAAGAAAGCAATCTAAAGTCTTCTCTCCGAGCCACTCTCCCTC	557
Qy	301	tgacaattgtagaaactcgcgcgcacagggagagccgagatgtlatgaltctcagcaaatcg	360
Db	556	TGACAAATTGTAGAAAAACCTCGCGCCACGGGAAAGGCCGAGATTGTATGATCTCAGCAAACTCG	497
Qy	361	cgagtgttgaagatctcggcgcccaacctggtgcatacaactgtttgctgtccaagtgtcga	420
Db	496	CGAGTGTGGAAGTTCTTGCGCCACCCCTGGTCTCAATACACTGTTTCCGCAAGCTGTCGA	437
Qy	421	aacaaataaaacaagacacacgaatgaattccgtcagttgagacttggatcttcgttaacacaa	480
Db	436	AACCATATTAACACGACACGATGAATTTCTCTCAGTGGGACTTGGATTTTGTATACACACA	377
Qy	481	atctcatctgcacaaggttgtctccagtttgttagcaggagatalcagtcaccaacccaatvgaga	540
Db	376	ATCTCATCTGCCAAAGAGTTGTTCCAGTTGTATACAGAGATATCATGACCAACCAATGAGA	317
Qy	541	tattctcgaggttgaaggttgcctgagacttggaaacatctggtatccaccataaaccaagta	600
Db	316	TATTCTCGAGGTGAGGGTGTCTAGGAGTTGGAACTCTGGATCCACATTAACCAAAAGTA	257
Qy	601	tagaagatccctgaaggtctctcccaaccaatctcaactcttggtctgttcttgaacctgaa	660
Db	256	TAGAAGTTCCTGAGGTCTTCTCCACCAATCTCAACTCTGTGGCTGTGTTTAACCTGAGAA	197
Qy	661	ggccttagatccaaagcaatagtcacactctctcttggccataagtaaccttagagtgat	720
Db	196	GGCCTTAGATCCAAACCCATTAGTACACTCTTGGCCATTAAGTAACCTTTAGAGTGATTT	137
Qy	721	gactcatcctaagcagatcaagaagctctcccaacaactctgacttaataaagaggtctct	780
Db	136	GATCTATTAAACGGATCAAGAACTCTCCAAACAACCTGCTTACTATTAAAGGGTCTCTT	77
Qy	781	atattatagacatcttbgactcttgaacaaacctgctgtcgtatctccctgcagcccgagg	840
Db	76	ATATTATTAGACATCTTGTGATCTTGAACAACCTCGTGTGAATTTCTCGAGCCCGGGG	17
Qy	841	atccactagctctaga	856
Db	16	ATCCACTAGTCTCTAGA	1

RESULT 3
 US-07-644-372-1/G
 ; Sequence 1, Application US/07644372
 ; Patent No. 5416009
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazzeri, Mario E.
 ; APPLICANT: Nutman, Thomas B.
 ; APPLICANT: Weiss, Niklaus
 ; TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
 ; TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGEN
 ;
 ; NUMBER OF SEQUENCES: 2
 ;
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 ; STREET: 1615 L. Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ;
 ; ZIP: 20036
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/644,372
FILING DATE: 19910123
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 52..507
US-07-644-372-1

Query Match      8.48; Score 71.8; DB 1; Length 822;
Best Local Similarity 51.38; Pred. No. 4.2e-10;
Matches 217; Conservative 0; Mismatches 202; Indels 4; Gaps 2;

QY 294 ctccctcgacaattgtagaanaactgcgcgcagcgagagccgagattgtatcgaagc 353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 637 CTCATGTTTACGCTCGAAGAGATTCCGCACTGGATTTCGCAAGATGATGTTGTTTGC 578
QY 354 aaactcgagagtggtgaagtcgtgcg---ccacctggtgacatactgtttgcctgcg 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 577 AAATCCATTAAGCTTTGAAATTTCCGCGATTTCCCGCATGTTGAGTATCCGATACCTTC 518
QY 411 aagctgcgaacaataaacaacagacagatgaatccctgcagctggagcttgatttc 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 517 AGGTGTTTAAACCAAGATATACATAGATGAAGTCTGCTGCTTTCGTGGACCTGA 458
QY 471 gtaacacacatctcatctgcagcaagctgtg--ttccagctgtagcagagatcatcaacca 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 457 TCCATATATAGATTAACACTGTCGCACTGCTAATTTTGCCGAATATTAATTTTCA 398
QY 530 accaatgagatatctcgcgaggtgaggtgtgctaggaacttgacaactcgtgacacca 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 ACCAATGTGTCACACTCTGTAATACGGGGTTTTTCAGATGCGTCCGAGTACAGTCA 338
QY 590 taacctgaagatagaagttcctgcaggtctctccaccaactcgaactcgtgactgttt 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 337 TAACGAGCGTATTAAGGCTCCAGGTTCCGATCCCATGATTAATTTGTGGGCTGATTC 278
QY 650 gaacctgagaagccttagatccaagccatagtcacactcctctcttgccataagtaact 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 277 TTACTCTCGTCGGCGTGAAGTTCAATGCCCCAGATTACCGTGAGATTTATTGTAACAT 218
QY 710 tta 712
    |||
DB 217 TGA 215
```

```
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STERNE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-948A-3

Query Match      5.58; Score 47; DB 2; Length 2185;
Best Local Similarity 90.98; Pred. No. 0.0022;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 802 ctgacaacactgctgaatcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2018 CTCACCAACACTGTCGCGAATTCGACGCCGCGGAGATCACTAGTTCTAGA 2072

RESULT 5
US-08-467-947A-3
Sequence 3, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPRI
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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US-08-482-130C-60

Query Match

5.5%: Score 46.8; DB 2; Length 234;

Best Local Similarity 73.2%: Pred. No. 0.0011; Mismatches 22; Indels 0; Gaps 0;

Matches 60; Conservative 0;

Oy 775 tctcttattatagacactcttgatcttgaacaacctcgtgtgaattccctgcagcc 834

Db 129 TATCTTGTAAAGATGAGAGCGCGCTCAATCCAAACGCTGTCGCAATTCTGCAAGC 70

Oy 835 cgggggagatccactagtcttaga 856

Db 69 CGGGGATCCACTAGTCTTAGA 48

RESULT 8

US-08-484-211C-60/c

Sequence 60, Application US/08484211C

Patent No. 5972645

GENERAL INFORMATION:

APPLICANT: Grieve, Robert B.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wu Hunter, Shirley

APPLICANT: Frank, Glenn R.

APPLICANT: Stiegler, Gary L.

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sheridan Ross P.C.

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,211C

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-25-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 234 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..234

US-08-484-211C-60

Query Match 5.5%: Score 46.8; DB 2; Length 234;

Best Local Similarity 73.2%: Pred. No. 0.0011; Mismatches 22; Indels 0; Gaps 0;

Matches 60; Conservative 0;

Oy 775 tctcttattatagacactcttgatcttgaacaacctcgtgtgaattccctgcagcc 834

Db 129 TATCTTGTAAAGATGAGAGCGCGCTCAATCCAAACGCTGTCGCAATTCTGCAAGC 70

RESULT 10

Oy 835 cgggggagatccactagtcttaga 856

Db 69 CGGGGATCCACTAGTCTTAGA 48

RESULT 9

US-08-906-769-60/c

Sequence 60, Application US/08906769

Patent No. 6077687

GENERAL INFORMATION:

APPLICANT: Grieve, Robert B.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wu Hunter, Shirley

APPLICANT: Frank, Glenn R.

APPLICANT: Stiegler, Gary L.

APPLICANT: Gaines, Patrick J.

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,769

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/639,075

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-25-C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 234 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..234

US-08-906-769-60

Query Match 5.5%: Score 46.8; DB 3; Length 234;

Best Local Similarity 73.2%: Pred. No. 0.0011; Mismatches 22; Indels 0; Gaps 0;

Matches 60; Conservative 0;

Oy 775 tctcttattatagacactcttgatcttgaacaacctcgtgtgaattccctgcagcc 834

Db 129 TATCTTGTAAAGATGAGAGCGCGCTCAATCCAAACGCTGTCGCAATTCTGCAAGC 70

Oy 835 cgggggagatccactagtcttaga 856

Db 69 CGGGGATCCACTAGTCTTAGA 48

RESULT 10


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-639-075A-60

Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0011;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy 775 tctctatattatagacatcttgcattcttgaaacaaacctgctgctgaattccctcagcc 834
129 TATCTTGTAAGATGAGCGCGCTCATATCCAAACCAACGCTCTGCGGAATTCCTCAGCC 70

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DR NPI: 1999-611305/52.
 DR P-PSDB: AAY49098.
 XX
 XX
 FT New flowering locus T polypeptide that regulates flowering time,
 FT particularly used to accelerate flowering -
 PT
 PS
 XX Claim 5: Fig 2: 64pp; English.
 CC
 CC This sequence is the flowering locus T (FT) gene of *Arabidopsis thaliana*.
 CC FT regulates flowering in plants by modulating flowering time.
 CC Overexpression of FT results in early flowering, while loss of function
 CC mutations or antisense directed to FT causes late flowering. The FT
 CC polypeptide has a molecular weight of approximately 20kD, and is located
 CC on chromosome 1. The FT polypeptide is used in the invention to modulate
 CC flowering time in many mono and di-cotyledonous plants. The FT
 CC polynucleotide sequence is used for recombinant production of the
 CC polypeptide, and as a source of antisense, ribozyme or triplex forming
 CC sequences. The FT polypeptide can also be used to raise antibodies and to
 CC screen for modulators or cellular binding proteins. The methods of the
 CC invention allow for the production of crops at any time of year.
 XX
 XX Sequence 856 BP; 263 A; 150 C; 194 G; 249 T; 0 other;
 50

Query Match	100.0%;	Score 856;	DB 20;	Length 856;
Best Local Similarity	100.0%;	Pred. No. 2.9e-190;		
Matches 856;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	ctgaagttttttttttttttttttttttaaatataaacacttcaattcaatgaatgaataa	60
Db	856	CTCGAGTTTTTTTTTTTTTTTTTTTTTAATAATATAACATTTCATTCATGATTTATA	797
OY	61	taattatcgcatcacacactalaaaglaaanaacttcatttcctcccccctcaatt	120
Db	796	TAATTAATGCGATCACAACGATATAAAGTAAACACTCTCATTTTCCGCCCTCATTT	737
OY	121	ttattacaacttatattgaactactatagagatcatcaacgcttcgttaactcgatca	180
Db	736	TTATTACACACTTATATATTTGAACCTACTATAGGCATATACCGTTGCTACTCGATCA	677
OY	181	taaaatcgltataaatlaaaatactatagaatgcaataatcctcaaglatgcaaat	240
Db	676	TAAATGGTTTAAATTTAAATTAATCTATAGATGCATTAATCTCATGAGATTAAGCAATAT	617
OY	241	caattggtataaaagaaagacatctaaagtccttcctcccgacacatccctc	300
Db	616	CAATTGGTTATATAAAGGAAGAAGCAGCATATAAGCTTCTTCCCTCGCGACGACATCCCTC	557
OY	301	tgacaaatgtgaaanaactcgcgcgcaggggaagcgcgagatgtagactcgaacaaatcg	360
Db	556	TGACAAATTTGTAAACTGCGCGCCACGGGAAGGCCGAGATTGTATGATCTACGMAACTCG	497
OY	361	cgaagtgltgaaagttctgcgcgcacccctgtgtacatactgttctcgtcgaacgtgcga	420
Db	496	CGAGTGTGAGAGTTCTGGCGCCACCCCTGCTCATACACTGTTTCCGCCCAACTGTGCA	437
OY	421	aacaatlaaacaagaagaatgaattcctgcgcagtgagattgatttgcgtaacaca	480
Db	436	AACATATATAAACGACGACGATGATATCTCGCACTGGGACTTGATTTGTAAACACACA	377
OY	481	atccatattgccaaaaggttggttcacagttgtatgcagaagatalcagtlcacaacaatgaga	540
Db	376	ATTCATATTGCCAAAGGTTGTTCCAGTTGTACAGAGGATATACGACACCAACCAATGAGA	317
OY	541	tattctcggaggatgagggttgctgagacttggaaacatctggatccaccataacccaagta	600
Db	316	TATTCTCGAGGTGAAGGTTGCTGTAGGACTTGGAACATCTGGATCCACCATTAACCAAGTA	257
OY	601	tagaagttcccggaaggtctctcccaacaatctcaactcttgcttggtttgaacctgaga	660
Db	256	TAGAAGTTCGAGAGTCTTCTCCACCAATCTCACTCTGGCTTGTTTAACCTTGAA	197

[illegible]

RESULT 2

ID	AAZ28491	standard; cDNA; 856 BP.
1	ATG	1
2	ATG	2
3	ATG	3
4	ATG	4
5	ATG	5
6	ATG	6
7	ATG	7
8	ATG	8
9	ATG	9
10	ATG	10
11	ATG	11
12	ATG	12
13	ATG	13
14	ATG	14
15	ATG	15
16	ATG	16
17	ATG	17
18	ATG	18
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49	ATG	49
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57	ATG	57
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92	ATG	92
93	ATG	93
94	ATG	94
95	ATG	95
96	ATG	96
97	ATG	97
98	ATG	98
99	ATG	99
100	ATG	100

AC AAZ28491;

DT 17-JAN-2000 (first entry)

DE Flowering locus T (FT) gene antisense insert.

KW Flowering locus T gene; FT; flowering time; modulator; early flowering; anti-bodv; cellular binding protein; cross; antisense construct; ss

XX
XX

XX
DN E000953070-A1XX
XX
21-OCT-1999

XX 13-APR-1966.

XX
15-APR-1969.XX
XX
/SAIR) SAIR INST BIOLOGICAL STUDIESXX
PT
Weiss, D.

XX WPT : 1000-611305/53
DP

XX
DT New flowering locus T polynatide that regulates flowering time.

PT particularly used to accelerate
XY

PS Example 2; Fig 3; 64pp; English.

This is the flowering locus T (FT) gene antisense polynucleotide sequence. This sequence is used in the production of the antisense construct of the invention pSK1060. FT regulates flowering in plants by modulating flowering time. Overexpression of FT results in early flowering, while loss of function mutations or antisense directed to FT causes late flowering. The FT polypeptide has a molecular weight of approximately 20kD, and is located on chromosome 1. The FT polypeptide is used in the invention to modulate flowering time in many mono and di-cotyledonous plants. The FT polynucleotide sequence is used for recombinant production of the polypeptide, and as a source of antisense, ribozyme or triplex forming sequences. The FT polypeptide can also be used to raise antibodies and to screen for modulators or cellular binding proteins. The methods of the invention allow for the production of crops at any time of year.

Sequence 856 BP; 249 A; 194 C; 150 G; 263 T; 0 other;

Query Match	100.0%	Score 856;	DB 20;	Length 856;
Best Local Similarity	100.0%	Pred. NC 2.9e-190;		
Matches 856; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	ctcgagttttttttttttttttttttttataataaataacacttcatttcagttagattaata	60	KW	metabolic pathway; promoter; termination sequence; ss
XX				XX	
OS	1	ctcgagttttttttttttttttttttttataataaataacacttcatttcagttagattaata	60	OS	Arabidopsis thaliana.
QY	61	taattatcgatcacacactatataaagtaaacacttcatttcctcccccctcattt	120	PN	EPI033405-A2.
XX				XX	
DB	61	taattatcgatcacacactatataaagtaaacacttcatttcctcccccctcattt	120	PD	06-SEP-2000.
XX				XX	
QY	121	ttatatacacttlatatattgaactactatagagcatcatcacggttcgttaactcgatca	180	PF	25-FEB-2000; 2000EP-0301439.
XX				XX	
DB	121	ttatatacacttlatatattgaactactatagagcatcatcacggttcgttaactcgatca	180	PR	25-FEB-1999; 99US-0121825.
QY	181	taaaatgggttacttaataaataactatagatgcataaataatcatcagagtatgcataat	240	PR	05-MAR-1999; 99US-0123180.
XX				PR	09-MAR-1999; 99US-0123548.
DB	181	taaaatgggttacttaataaataactatagatgcataaataatcatcagagtatgcataat	240	PR	23-MAR-1999; 99US-0125788.
XX				PR	25-MAR-1999; 99US-0126264.
QY	241	caattggttataaagggaagagcatataagttcttctctccgcagccactctccctc	300	PR	29-MAR-1999; 99US-0126785.
XX				PR	01-APR-1999; 99US-0127242.
DB	241	caattggttataaagggaagagcatataagttcttctctccgcagccactctccctc	300	PR	06-APR-1999; 99US-0128234.
XX				PR	08-APR-1999; 99US-0128714.
QY	301	tgcacatttgttgaanaacgtcgccagcggaagcgcgagatgttagatctcagcaaatcg	360	PR	16-APR-1999; 99US-0129845.
XX				PR	19-APR-1999; 99US-0130077.
DB	301	tgcacatttgttgaanaacgtcgccagcggaagcgcgagatgttagatctcagcaaatcg	360	PR	21-APR-1999; 99US-0130449.
XX				PR	23-APR-1999; 99US-0130510.
QY	361	cgaagtgttgaagttctcgcgcacacctggtgtacacactgtttgctcgcgaacgtctcga	420	PR	23-APR-1999; 99US-0130891.
XX				PR	28-APR-1999; 99US-0131449.
DB	361	cgaagtgttgaagttctcgcgcacacctggtgtacacactgtttgctcgcgaacgtctcga	420	PR	30-APR-1999; 99US-0132048.
XX				PR	04-MAY-1999; 99US-0132407.
QY	421	aacataataaacacagacacagatgaattccctgcagtgagacttggatttcgttaacacac	480	PR	05-MAY-1999; 99US-0132484.
XX				PR	05-MAY-1999; 99US-0132485.
DB	421	aacataataaacacagacacagatgaattccctgcagtgagacttggatttcgttaacacac	480	PR	06-MAY-1999; 99US-0132486.
XX				PR	07-MAY-1999; 99US-0132487.
QY	481	atccattgcgaagaaggtgtgtccagttgttgcagcaaggaatcatcagtcaccaacgaatgaga	540	PR	07-MAY-1999; 99US-0132863.
XX				PR	11-MAY-1999; 99US-0134256.
DB	481	atccattgcgaagaaggtgtgtccagttgttgcagcaaggaatcatcagtcaccaacgaatgaga	540	PR	14-MAY-1999; 99US-0134218.
XX				PR	14-MAY-1999; 99US-0134219.
QY	541	tattctcggagggtgagggttgcaggaacttggaaacatctgcgataccaccaataacgaagta	600	PR	14-MAY-1999; 99US-0134221.
XX				PR	14-MAY-1999; 99US-0134221.
DB	541	tattctcggagggtgagggttgcaggaacttggaaacatctgcgataccaccaataacgaagta	600	PR	18-MAY-1999; 99US-0134370.
XX				PR	18-MAY-1999; 99US-0134768.
QY	601	tagaaggttcctcggaaggtctctccacccaactccaactctggtctgttttgaaccttagaa	660	PR	19-MAY-1999; 99US-0134941.
XX				PR	20-MAY-1999; 99US-0135124.
DB	601	tagaaggttcctcggaaggtctctccacccaactccaactctggtctgttttgaaccttagaa	660	PR	21-MAY-1999; 99US-0135353.
XX				PR	24-MAY-1999; 99US-0135629.
QY	661	ggccttagatcacgaagcatagtcacactctctcttgcgcataagtaacctttagagatt	720	PR	25-MAY-1999; 99US-0136021.
XX				PR	28-MAY-1999; 99US-0136782.
DB	661	ggccttagatcacgaagcatagtcacactctctcttgcgcataagtaacctttagagatt	720	PR	01-JUN-1999; 99US-0137222.
XX				PR	03-JUN-1999; 99US-0137528.
QY	721	gatctatataaacygatacaagaagctctccacaacactctgcttactataagaagggtctctt	780	PR	04-JUN-1999; 99US-0137502.
XX				PR	07-JUN-1999; 99US-0137724.
DB	721	gatctatataaacygatacaagaagctctccacaacactctgcttactataagaagggtctctt	780	PR	08-JUN-1999; 99US-0138094.
XX				PR	10-JUN-1999; 99US-0138540.
QY	781	atatttataagacatctttagatcttgcagaacaacctcgtgcgaattctcgtcagccggggg	840	PR	10-JUN-1999; 99US-0138847.
XX				PR	14-JUN-1999; 99US-0139119.
DB	781	atatttataagacatctttagatcttgcagaacaacctcgtgcgaattctcgtcagccggggg	840	PR	16-JUN-1999; 99US-0139452.
XX				PR	16-JUN-1999; 99US-0139453.
QY	841	atccactagttcttaga	856	PR	17-JUN-1999; 99US-0139492.
XX				PR	18-JUN-1999; 99US-0139454

PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 15-JUL-1999; 99US-0144005.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145919.
PR 27-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
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PR 27-AUG-1999; 99US-0151060.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.

PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
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PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 80.9%; Score 692.4; DB 21; Length 775;
Best Local Similarity 99.9%; Pred. No. 4e-152;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 119 ttltatcacacttatatatgaactactataggcatcatcaaccgttcgttactcgtat 178
DB 758 ttttttttACACACTTATATATGAACTACTATAGCATCATCACCGCTTACTCGTAT 699
OY 179 cataaatggttataatataatcactatagatgcataaatctcraaagtatgcat 238
DB 698 CATTAATGTTATTATAAAGTAAGTATGATCATTAATCTCATATAGATGATGCAT 639
OY 239 atcaattggtlataaaggaaagccatcaaatgctcttcctccgagccactctccc 298
DB 698 ATCAATTTGGTTATAAAGGAGAGCCATCTTAAGCTTCTTCCGAGCCACTCTCCC 579
OY 299 tctgacaattgtagaaaacgcgcgcacggaagcgagatcgtlagaletcagaacact 358
DB 578 TCTGACAATTTGAGAAACTCGCGCCACGCGGAGGCGGAGATTGATCTTCACGAACT 519
OY 359 cgcgagtgltgaagttcgcgcgcacccctggtgcataacacglttgcctgcagaactc 418
DB 518 CGCGAGTGTGAAGTTCTGCGCCACCTGTGCTATACCTGTTGCTCCCAAGCTTCTC 459
OY 419 gaaacaatataaacacgacacgatgaattcctgcagtggaacttgatcttcgtataaca 478
DB 458 GAACCAATATAACACGACGATGATTTCTCGAGTGGAGCTTGATTTTCGTATACACA 399

Qy 479 caatcctatgccaaggltgttccagltgttagcaggatatacagtcaccaaccaatgga 538
|||||
Db 398 CAATCTATTCGCCAAGGTTGTTCCAGTGTAGCAGGAGATATCAATCAACCAATGGA 339
Qy 539 gatattctcgagggtgaaggtgtgtcaggacttggacaacatctggatccacataacaaag 598
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Db 338 GATATTCCTCGAGGAGGAGGTTGCTAGAGACTTGGAACTCTGGATCCACCAATAAACCAAG 279
Qy 599 tatagaattctcttagagctcttcacacaatcacaactctggctgtgtttggaactag 658
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Db 278 TATGAAGTTCTCTGAGGCTTCTCCACCAATCTCAACTCTGGCTGTGTTTGAACCTGAG 219
Qy 659 aaggccttagatccaagcattagtcacactctcttggccataaagtaaccttaagtcga 718
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Db 218 AAGGCTTAGATCCAAAGCCATTAGTCACCTCTCTTGGCCATAATACCTTTAGAGTGA 159
Qy 719 ttgatctataaaggatcaagaacgcttccaacaactctcttaacttaagaaggtctc 778
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Db 158 TTGATCTATTAAACGAGTCAAGAACGCTCCAAACAACCTGCTTACTATAGAGGCTCTC 99
Qy 779 ttatattatagacactctttagctcttgacacaac 812
|||||
Db 98 TTATATTATAGACATCTTTGATCTTGAACAAC 65

RESULT 4
AAC48359/c
ID AAC48359 standard; DNA: 754 BP.
XX
AC AAC48359;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134370.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 24-JUN-1999; 99US-0140695.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 06-JUL-1999; 99US-0142390.
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PR 09-JUL-1999; 99US-0142920.
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PR 20-JUL-1999; 99US-0144352.
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PR 25-OCT-1999; 99US-0161405.

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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 80.8%; Score 692; DB 21; Length 754;
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Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 ttattacacctatataattgaactaiaaggaatcaccgttcgttactgtatca 180
DB 754 TTATTACACACTTATATATTTGAATCTATAGCATCAACCGTTCCGTACCTGATCA 695
QY 181 taaatgtgtattaataataataactatagatgacataatccatcagatgtgaaatat 240
DB 694 TAAATGTTATTAATAATTAATAATCTATAGCATCAATCAATCAATCAATCAATAT 635
QY 241 caattggtataaagaagaagccatctaaagtctctctcccgagccactctccctc 300
DB 634 CAATTGTTATTAAGGAAGAACCAATCTAAAGTCTTCTCCCGCAGCACTTCCCTC 575
QY 301 tgacaattgtagaaaacttgcgcacagggaaagccgagatgttagatctcagaacctcg 360
DB 574 TGACAAATTTAGAAAACTCGCGGCCACGGGAAAGCCGAGATTTGATATCTACACAACTCG 515
QY 361 cgaagtgtgaagttcttgcgcaccccttgcgcacacatggttgcctgcgcagagctgtcga 420
DB 514 CGAGTGTGAAGTCTCGGCGCACCCGTGTGATACACTGTTGCTGCGCAAGCTGTGCA 455
QY 421 aacaatataaacaagacagatgaatctcctgcagtgcgtggaacttgcgttaacacaca 480
DB 454 AACCAATATAACACGACGACGATGAATTCCTCGAGTGGACTTGGATTTTCGTACACACA 395
QY 481 atcctatgccaaggttgcctccagtttgcagggatatacgttaaccaacaaatggaga 540
DB 394 ATCTCATTTGCCAAGGTTGCTTCAGTTGTAGCAGGATATCAGTCAACCAATGGAGA 335
QY 541 tatctcggaggttgaggggttgcctagacttgaacatcgtgaatccaacaaacaaagta 600
DB 334 TATTCTCGAGGTGAGGGTTCGTAGACTTGGAACTCTGGATCCACCACTAACCAAGTA 275
QY 601 tagaagttccctgaggtctctccaccacatcacaactctgtgcttgcgttgcgtgaaga 660
DB 274 TAGAAGTTCCTGAGGCTTCTCCACCAATCTCAACTCTTGCTGTTTGAACCTGAGAA 215
QY 661 ggccttagatccaagccatagtaacctctcttggccataagtaacctttagatgatt 720
DB 214 GGCCTTAGATCCAAAGCCATTAATGATCACTCTTTGGCCATTAAGTAACCTTTAGAGTAT 155
QY 721 gactcatiaaaggatcaagaagctctccaacaactctctactataaagaggtctct 780
DB 154 GATCTATTAAAGGATCAAGAACGTCCTCAACAACCTCTCTTATATAGAGGGTCTCT 95
QY 781 atattatagacactcttgcattcttgaacaac 812
DB 94 ATATTATATAGACATCTTGTATCTTGAACAAAC 63

RESULT 5
AAA60683/C
ID AAA60683 standard; DNA; 528 BP.
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AC AAA60683;
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DT 26-OCT-2000 (first entry)
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DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:2.
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KW Arabidopsis thaliana; Cruciferae; plant; control; flowering;

PR 18-JUN-1999; 99US-0139456.
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PR 28-JUN-1999; 99US-0140823.
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PR 13-JUL-1999; 99US-0143542.
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PR 29-OCT-1999; 99US-0162142.

Query Match 44.1%; Score 377.6; DB 21; Length 528;
Best Local Similarity 82.2%; Pred. No. 9.4e-79;
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DB 528 CTACGTTCTTCTTCCCCACAGCCATTCCTCTGGCAGTTGAAGTAAAGACGCCAC 469
QY 327 ggaagccgagatgtagatctcagcaactcgcgagtgttgaagttctggcgccacc 386
DB 468 AGCAAGACCAAGATTGTAGACTTCAGCAACACTCAGAGTGTGAAGTGTGGCGCCACCC 409
QY 387 tggtcataactcgttgcctccgcaagctgttcgaacaataataacaacgacagatgaat 446

OY 590 taaccaagaatagaagcttcgaggtctctccaccaatctaactcttgctgtttt 649
 Db 229 TCCAAAATGTGAAGGATCTGAGATCCACACATGAGATCTTACCCCTGGCTTGGAG 170
 OY 650 gaacctgaagaagcccttagatccaagccattagtcacccctcttgccataagtaacct 709
 Db 169 AATCAGAAAGAGAAAGACCTCATGGCCATTGGAGACTTGCCTTGTATTAACATCAT 110
 OY 710 ttagaatgatgatctattaaacgatacaagaacgctcccaaacctctctaactaa 769
 Db 109 TCATCTTACTGTTGGAGTGAAGAAATCAAGAACATCTCTACACACTCTCCCATTTTCA 50
 OY 770 gaaggctctctattattataagacatctt 797
 Db 49 ATGGCTCTATCACCTTAGTCCCATATT 22
 RESULT 10
 AAC90668/C
 ID AAC90668 standard; cDNA; 519 BP.
 XX AAC90668;
 XX
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 DT 20-MAR-2001 (first entry)
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 DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 43.
 XX
 DE Strawberry: flowering regulation; floral homeotic gene; field crop;
 KW harvesting; fruit production; ss.
 XX
 OS Fragaria vesca.
 OS
 PN WO200071722-A1.
 PD 30-NOV-2000.
 XX
 PE 24-MAY-2000; 2000MO-US14297.
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 PR 25-MAY-1999; 99US-0318789.
 PR 24-MAY-2000; 2000US-0318789.
 XX
 PA (DNAP) DNA PLANT TECHNOLOGY CORP.
 XX
 PI Oeller P, Guttererson N;
 XX
 DR WPI; 2001-025165/03.
 DR P-PSDB; AAB50271.
 XX
 PT Novel nucleic acid involved in controlling plant flowering processes is
 PT useful for generating transgenic plants, in particular strawberry
 PT plants having altered flowering behavior such as early, delayed or
 PT day-neutral flowering -
 XX
 PS Claim 23; Page 94-95; 97pp; English.
 XX
 CC The present invention provides the nucleic acid and protein sequences of
 CC a number of proteins from the strawberry which are involved in the
 CC regulation of flowering. These were identified using primers based on the
 CC homologous sequences from A. thaliana, B. napus and R. sativus. They can
 CC be used in the production of transgenic field crops whose flowering is
 CC regulated and the time of fruiting and harvesting can be manipulated.
 XX
 SO Sequence 519 BP; 143 A; 132 C; 120 G; 124 T; 0 other;

Query Match	18.8%;	Score 161.2;	DB 22;	length 519;
Best Local Similarity	57.3%;	Pred. No. 2.7e-28;		
Matches 292;	Conservative	0;	Mismatches 218;	Indels 0;
				Gaps 0;

QY 277 ctctcgcgacgacctctccctctgacattgtagaaacctggcgccacggaagcg 336
||| || | ||| ||| ||| ||| ||| ||| ||| ||| ||
Db 515 CGTCTTCCTTGCGCCGTTCTCTCTGTGCATTGAAGTAACGGCAGCAAGAACCCA 456

QY	337	agatgtgatcatcgaacaaactgcgcagtggttgaagttcttggcgccacctgtgtac	336
Db	455	AGGTGGTTTTCGGCGCCAAAGTTTCGGGTGTGTAAGTATCCCTTGAAGAAAGGGGGTTC	366
QY	397	actgttcgcgcgaagctgtgcgaacataataacagcacgatatcaatctgcgcagtg	456
Db	395	ACCGACTCCCTTCGTTTTCGATGAAGAGAACMAACAACTCTGTGATGCCATATGTTT	358
QY	457	ggacttgatcttcgtaacacacaatctcaltgcgaagtglttcagttgtgaaggg	516
Db	335	GGCCTTGGCATCTCCTACTCACCACCTTCTTCCAAATGAGCATCTGTGTGCCAGGA	276
QY	517	atatacgcacacaacaaatgagatattctcggagggtgcgttcagagcttgcagaca	576
Db	275	AGTGTGTGCACATCCAGATGACGAGTGTCTTTCAAAATGAGATCACTAAGGCCAGGACA	216
QY	577	tctgaatccacacaaacaaagataagaattcctcgtgagttcttcacacaatcact	636
Db	215	TCTGGTCTGTCAATACCAAGATGAAGATGATCTCATGTGCGCTCTGAAATCTCAAT	156
QY	637	cttgacttggttttgaacctctggaagagcctatgatccaaagccatatagtcactcttgg	696
Db	155	CTAGGTTTGGCGGTACTCGACGAAGAGGAAAGCTCATGTCATTGACAGACAGCTTCTCG	96
QY	697	ccataagtaaacctttagaagtatgatcatataacagatcaagaagtcgtccacaact	756
Db	95	TTGTAAAGACACATCATTTTGTAGTGGGGGTGAAGAAATCAAAACATCTCTTAATGACT	36
QY	757	ctgcttaactataaagggtctctataatt	786
Db	35	CTTCCACAGCTAGAGGTTCCGACATTTCTT	6

RESULT	11
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ID	AAV66749 standard; DNA; 4512 BP.
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AC	AAV66749;
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DT	02-FEB-1999 (first entry)
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DE	Arabidopsis pathogen response gene LSD1.
XX	
KM	LSD1: plant pathogen response; apoptosis; programmed cell death
KM	disease resistance; herbicide resistance; transgenic plant;
KM	crop protection; ss.
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OS	Arabidopsis thaliana.
XX	
FH	Key
FT	CDS
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FT	2371..2494
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FT	/number=1
FT	2495..2583
FT	/*tag= c
FT	/number=1
FT	2584..2688
FT	/*tag= d
FT	/number=2
FT	2689..3177
FT	/*tag= e
FT	/number=2
FT	3178..3317
FT	/*tag= f
FT	/number=3
FT	3318..3417
FT	/*tag= g
FT	/number=3
FT	3418..3490
FT	exon

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ET      /*tag= h
ET      /number= 4
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ET      insertion, which alters the reading frame"
ET      intron
ET      3491..3582
ET      /*tag= 1
ET      /number= 4
ET      exon
ET      3582..3658
ET      /*tag= j
ET      /number= 5
ET      intron
ET      3659..3746
ET      /*tag= k
ET      /number= 5
ET      exon
ET      3747..3783
ET      /*tag= 1
ET      /number= 6
XX
XX      W09837755-A1.
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XX      03-SEP-1998.
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XX      27-FEB-1998; 98WO-US04077.
XX
XX      28-FEB-1997; 97US-0039063.
XX
XX      (UNNC-) UNIV NORTH CAROLINA.
XX
XX      Dangel JL, Dietrich RA, Epple PM, Rieberg MH;
XX
XX      WPI: 1998-531501/45.
XX      P-PSDB: AAW72366-67.
XX
XX      New isolated Arabidopsis genes - useful for producing transgenic
XX      plants which show resistance to cell death caused by pathogens or
XX      herbicides.
XX
XX      Claim 2; Page 34-38; 88pp; English.
XX
XX      This is the nucleotide sequence of the wild-type LSD1 gene of
XX      Arabidopsis thaliana. It includes exons encoding an LSD1
XX      polypeptide (see AAW72366-67) that has an effect in regulating the
XX      initial response of plants to pathogens and the subsequent spread
XX      of plant cell death engendered by infection. LSD1 functions to
XX      monitor levels of superoxide-dependent signal and negatively
XX      regulates a plant cell death pathway. To isolate the gene and
XX      LSD1 cDNA (see AAW66750-51), Arabidopsis mutants were obtained which
XX      exhibited constitutive cell death in the absence of pathogens. The
XX      lesion stimulating disease resistance or LSD phenotypes, which
XX      provided resistance to cell death, was then analysed by genetic
XX      and physical complementation studies. The sequences obtained were
XX      then compared to databases. The invention provides LSD1
XX      polypeptides and isolated DNA sequences, a transformation vector,
XX      mutated LSD1 DNA sequences, and a transgenic plant expressing LSD1
XX      mutant genes that affect resistance to herbicidal compounds or
XX      plant pathogens that normally result in plant cell death. Also
XX      claimed are LSD1-like (LSD1 and LSD2) proteins (see AAW72380-81) and
XX      proteins that interact with LSD-1 (see AAW72384-96). Products of the
XX      invention can be used to produce plants that show resistance to
XX      cell death caused by pathogens or herbicides.
XX
XX      Sequence 4512 BP; 1385 A; 819 C; 767 G; 1539 T; 2 other;
SQ
Query Match 17.0%; Score 145.8; DB 19; Length 4512;
Best Local Similarity 77.3%; Pred. No. 1.8e-24;
Matches 177; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Oy 560 gattccacataccaagaatagaagtctctgagctctccccaactccaactctt 639
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Db 122 gaaagaaatcaccaaggtgtgaagaattctcgaagtcgtccccaactccaactatt 181
Oy 640 ggcctgtttgaactggaagagccttagatccaagccattgtcacctctctttggcca 699
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Oy      700 taagtacaccttaagatgtatctatcatcaacgagatcaagaagcgtccacaactctg 759
    ||||| ||||| |||| | ||| | ||||| ||||| ||||| ||||| |||||
Db      242 taagtacaccttaagagagacccaacctcgtgaagagatcaagaacatccacaactcgt 301
Oy      760 ctactataagagaggtctctatattatagacatcttgatcttgaac 808
    | | | | ||||| |||| | ||| ||||| |||| | |||
Db      302 ccgaccagcagagagatcctctacgaacttaagacatatattacttggatc 350
RESULT 12
AAAT60139/C
ID      AAAT60139 standard; cDNA; 929 BP.
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XX      AAAT60139;
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XX      24-JUN-1997 (first entry)
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XX      Antirrhinum centroradialis gene cDNA clone.
XX
XX      Centroradialis gene; cen gene; flowering; transgenic plant; ss.
XX
XX      Antirrhinum majus.
XX
XX      Key Location/Qualifiers
XX      CDS 91..636
XX      FT /*tag= a
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XX      W09710339-A1.
XX
XX      20-MAR-1997.
XX
XX      13-SEP-1996; 96WO-GB02276.
XX
XX      13-SEP-1995; 95GB-0018731.
XX
XX      (INNE-) INNES CENT JOHN.
XX
XX      Bradley DJ, Carpenter R, Coen ES,
XX
XX      WPI: 1997-202235/18.
XX      P-PSDB: AAW13944.
XX
XX      Antirrhinum majus centroradialis gene and Arabidopsis homologue,
XX      Tfl1 - control switching of apical meristem to floral fate, useful
XX      in plant hybridisation and in control of growing season
XX
XX      Claim 1; Fig 4a; 83pp; English.
XX
XX      A cDNA clone (AAAT60139) codes for the centroradialis (CEN) protein
XX      (AAW13944) of Antirrhinum majus. It was obt'd. from a cDNA library of
XX      young inflorescences by RT-PCR. A genomic cen gene sequence
XX      (AAAT60141) was also obt'd. The wild-type role of the cen gene is to
XX      prevent the apical meristem from switching to a floral fate. The
XX      flowering characteristics of transgenic plants, esp. switching of
XX      apical meristem to a floral fate and the timing of flowering, can
XX      be manipulated by regulating cen gene expression. The cen nucleic
XX      acids can also be used as probes to isolate homologous genes, e.g.
XX      the terminal flower1 (tfl1) gene (see also AAAT60142) of Arabidopsis.
XX
XX      Sequence 929 BP; 274 A; 175 C; 198 G; 282 T; 0 other;
SQ
Query Match 13.6%; Score 116; DB 18; Length 929;
Best Local Similarity 54.5%; Pred. No. 1.1e-17;
Matches 289; Conservative 0; Mismatches 220; Indels 21; Gaps 2;
Oy      268 taagtctctctctccgcagcaactctccctctgacaattgagaanaactcgcgccag 327
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Db 581 GGAGGCCCAATTCATTTCTCTGTGTGAATTTCTCGGTGTAATCCATCCCTGCACACT 522
QY 388 ggtgcata-----cactgttgccgtcgaagctgtcgaacaataataacagaca 438
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Db 521 ACTGTGGGCTCAACATCGCTGCCCTCTTTCTCTGTGTGAACAGAAATACAAAC 462
QY 439 cgaatcttcctgcagtgaggacttggaatttcgtcaacacacacatctatgcgaagtt 498
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Db 461 CTGTGGATCCCTATGTTGCGCTTGCGCATTCATAGCTCACTACTCTTTCCCATAG 402
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RESULT 13

AAC90666/c
ID AAC90666 standard; DNA; 3696 BP.

AC AAC90666;

DT 20-MAR-2001 (first entry)

DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 37.

KW Strawberry; flowering regulation; floral homeotic gene; field crop;
harvesting; fruit production; ds.

OS Fragaria vesca.

PN WO200071722-A1.

PD 30-NOV-2000.

PF 24-MAY-2000; 2000WO-US14297.

PR 25-MAY-1999; 99US-0318789.

PR 24-MAY-2000; 2000US-0318789.

PA (DNAP) DNA PLANT TECHNOLOGY CORP.

PI 'Oeiller P, Guttersen N;

DR WPI; 2001-025165/03.

DR P-PSDB; AAB50269.

PT Novel nucleic acid involved in controlling plant flowering processes is
useful for generating transgenic plants, in particular strawberry
plants having altered flowering behavior such as early, delayed or
day-neutral flowering

PS Disclosure; Page 82-87; 97pp; English.

CC The present invention provides the nucleic acid and protein sequences of
a number of proteins from the strawberry which are involved in the

CC regulation of flowering. These were identified using primers based on the
homologous sequences from A. thaliana, B. napus and R. sativus. They can
be used in the production of transgenic field crops whose flowering is
regulated and the time of fruiting and harvesting can be manipulated.

XX Sequence 3696 BP; 1175 A; 618 C; 648 G; 1255 T; 0 other;

Query Match 9.6%; Score 82.6; DB 22; Length 3696;
Best Local Similarity 60.4%; Pred. No. 9.4e-10;
Matches 136; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 277 ctccctccgcagccactctccctcgtacacatgtagaacactgcgcgcggaagcg 336
Db 2636 CGTCTTCTTGAGAGAGATTCCCTCTGGGCAATTGAAGAAGACAGCACCGGAAGCCG 2577

QY 337 agatgtatgatctcagcaaacctcgcgagtggttgaagttcgtgcgcacccgtgtgcatac 396
Db 2576 AACTGTGTTGTTTTCGCAAACTTTCGAACTGTGCAATGTCCTTCGAAGGAGGAATC 2517

QY 397 actgttgccgcgaagctgtgcgaacaataataacacagacagatgattcctgcagtg 456
Db 2516 ACTGTCTGCTTACCTTTCTGTGTAACAAAAGAAACAAACCTGTGATCCCTATGTTT 2457

QY 457 ggacttgattctcgtlaacacacaatctcattgccaagtggtt 501
Db 2456 GGCTCGGCATTTTCAATTTTACACACCTCCCTTCCTGCAATTTT 2412

RESULT 14

AAT60142/c
ID AAT60142 standard; DNA; 1430 BP.

AC AAT60142;

DT 24-JUN-1997 (first entry)

DE Arabidopsis terminal flower 1 (tfl1) gene.

KW Terminal flower 1; tfl1 gene; centroradialis gene; cen gene;
flowering; transgenic plant; ss.

XX Arabidopsis thaliana var. columbia.

XX Key location/Qualifiers

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FT /codon_start= 235..237

FT intron 445..655

FT /*tag= b

FT exon 656..717

FT /*tag= c

FT intron 718..923

FT /*tag= d

FT exon 924..964

FT /*tag= e

FT intron 965..1051

FT /*tag= f

FT exon 1052..1430

FT /*tag= g

FT /*note= "in-frame stop codon at 1261-1263"

PN WO9710339-A1.

PD 20-MAR-1997.

PF 13-SEP-1996; 96WO-GB02276.

PR 13-SEP-1995; 95GB-0018731.

PA (INNE-) INNES CENT JOHN.

PI Bradley DJ, Carpenter R, Coen ES;

Search completed: September 14, 2002, 21:21:27
Job time: 13859 sec

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DEFINITION	Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds.			
ACCESSION	AB027504			
VERSION	AB027504.1	GI:4903011		
KEYWORDS	FT			
SOURCE	Arabidopsis thaliana (strain:landsberg er) cDNA to mRNA.			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
AUTHORS	1 (sites)			
TITLE	kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.			
JOURNAL	A pair of related genes with antagonistic roles in mediating flowering signals			
REFERENCE	Science 286 (5446), 1960-1962 (1999)			
AUTHORS	20050958			
TITLE	2 (bases 1 to 864)			
JOURNAL	Araki, T. and Kobayashi, Y.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences: Sakyo-ku, Kyoto, Kyoto 606-8502, Japan			
TITLE	(E-mail: tarague@r.bot.kyoto-u.ac.jp, Tel:81-75-753-4136, Fax:81-75-753-4141)			
FEATURES	Location/Qualifiers			
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	/map="90 cm on F5114"			
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	/gene="FT"			
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	/note="induces flowering; loss-of-function mutation delays flowering; similar to mammalian phosphatidylinositolamine binding protein (PEBP) and hippocampal cholinergic neurotransmitting peptide (HCNP) precursor"			
	/codon_start=1			
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Db	857	TTTTTTTTTTTTTAAAGTATTAATATTAACACTTCATTTGATGTATATATTA	798	
0y	67	tgcacatcacacataataaagtaaaacatctcatcttctcccccctcatcttattat	126	

D	b	797	TGCAATGCACACACTATTATAAGTAAACAACCTCATTTTCCTCCCTCCTCATTTTATTA	738
O	y	127	cacacttatataatggaactactatagcaatcacaacctgtcttactcgtaacataaat	186
D	b	737	CACACTTATATATGAAGTACTATGAGCGATCAACCGTTGGTACTGTATCATTAAT	678
O	y	187	ggattataatataataactatagatgcataaatacatcagaagtatgcaatatcaatg	246
D	b	677	GGTATTTAATTAATTAATCTATAGATGCTATTAATCTCATCACAGATATGCAATATCATG	618
O	y	247	gtttataaaggaaagaaacatatgaaggtcttcctccgcaaacactctcccttgaca	306
D	b	617	GTATTAAAGGAAGAAGAACCTTAAGGTCTTCTCCGCCAGACCACCTCCCTTGACAA	558
O	y	307	tgtgtaaaaactctgcggccaacgggaagccggaatttgtagatctcagcaactcgcga	366
D	b	557	TTGTGAAAACCTGCGGGCCACGGGAAGCGCGAATTGTAGATTTCAGACAACTCGGAGAG	498
O	y	367	ltgaagttctgagcgccaacctggtgataactgtttgcctgcgaagctgtcgaanaa	426
D	b	497	TTGAAGTCTTGCGCGCCACCCCTGCTCATACACTGTTCCTGCCCAAAGCTGTGAAACAT	438
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D	b	437	ATAAACAGACAGACGATGATTTCTGACAGGGGACTTGGATTTTCGTAACACCAATCTCA	378
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D	b	377	TTGGCAAAAGTTGTTCCAGTTGTACAGAGGATATCAGTACCAACCAATGAGATTTCT	318
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D	b	317	CGAGAGTAGAGGTTGCTAGGACTTGGACATCTGGATCCACCATTAACCAAGTATGAG	258
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D	b	257	TTCCTAGAGGTTCTTCCACCAATCTCAACTCTGTTCCTTTTGAACCTGGAAGGCCCT	198
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D	b	197	AGATCCAAGCCATTATGTACACCTCTCTTGGCCATATGATCACTTTAGATGATGATCTA	138
O	y	727	ttaaagcatcaagaagctctccaacaactctgctactactataagaaggctctatatt	786
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D	b	77	ATAGACATCTTGTACTCTTGAAACAAC	52
RESULT	4			
AY065378/c				
LOCUS	AY065378	840 bp	mRNA	linear
DEFINITION	Aribidopsis thaliana putative flowering signals mediating protein			PLN 11-DEC-2001
ACCESSION	AY065378			
VERSION	AY065378.1	GI:17529185		
KEYWORDS	FLI_CDNA.			
SOURCE	thale cress.			
ORGANISM	Aribidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Superrotia; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi			
	s. 1 (bases 1 to 840)			
	Yamada,K., Banno,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kaniya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,H., Meyers,M.C., Miranda,M., Natusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shimizu,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.			

TITLE	Full Length cDNA of gene Atlg65480 (GI:15218709)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 840)
AUTHORS	Yamada,K., Bann,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Teramichi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,D., Meyers,M.C., Miranda,M., Natsuka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE	Direct Submission
JOURNAL	Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PECC (SFP) Consortium members carried out the sequencing and annotation of the RALF cDNAs: Yamada, K., Banh, J., Chang, C. H., Cheng, E., Date, J. M., Gotsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Torluttini, M., Wu, H. C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Becker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologos, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES
source

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DEFINITION complete sequence.
ACCESSION AC001229
VERSION AC001229.1 GI:2182285
KEYWORDS HMG.
SOURCE HMG.
ORGANISM Thale cress.
Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 109560)
Vysotskaya,V.S., Osborne,B.I., Toriumi,M., Yu,G., Oji,O.,
Shen,Y.K., Buehler,E., Conway,A.B., Conway,A.R., Dewar,K., Feng,J.,
Kim,C., Kurtz,D., Li,Y., Shinn,P., Sun,H., Davis,R.W., Ecker,J.R.,
Fedorov,N.A. and Theologis,A.
The sequence of BAC F5114 from Arabidopsis thaliana chromosome 1
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 109560)
Theologis,A.
TITLE Direct Submission
AUTHORS Submitted (15-APR-1997) Plant Gene Expression Center, 800 Buchanan
JOURNAL Street, Albany, CA 94710, USA
REFERENCE 3 (bases 1 to 109560)
Theologis,A.
TITLE Direct Submission
AUTHORS Submitted (17-APR-1997) Plant Gene Expression Center, 800 Buchanan
JOURNAL Street, Albany, CA 94710, USA
REFERENCE 4 (bases 1 to 109560)
Theologis,A.
TITLE Direct Submission
AUTHORS Submitted (06-JUN-1997) Plant Gene Expression Center, 800 Buchanan
JOURNAL Street, Albany, CA 94710, USA
REFERENCE 5 (bases 1 to 109560)
Theologis,A.
TITLE Direct Submission
AUTHORS Submitted (11-JUN-1997)
COMMENT On Jun 10, 1997 this sequence version replaced gi:1943864.
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/translation="MDEVSTVNNENRKTMTIEPKKLRKRREPTAIENTLSEESQI
SLNLEMKGLDFYREVMDKSRDTDFSGSECSLSNVALMEBSLPSKLVDEI
YLKLEKTESTYMAVKSAYVSGRVSYGLNVDADVDLEDSESCIMCETRTDITM
PSSVAGVLKLRCTCKIHERITAVSAMLALQHEYTEKLMRSDLKAEKLGKILSE
VDIRFMDNMQKSSSEMAEKDSKEELKLOLEKNCEAKRKMERQVLEKIQ
QEKDEKLLQKAIVDENKKEETESRKRIKQODESEKQREKQAEKQLQVQK
QASIMERFLKSKSDSLQPKLPSEVTAQELSTKHENEIGKVVAIDNMFSTCEA
TVDDIRRYDLSPC"
10580..12759
/gene="F5114.3"
join(10580..10780,11596..11657,12371..12411,12536..12759)
/gene="F5114.3"
/note="Similar to Arabidopsis TFL1 (gb|U77674)."
/codon_start=1
/evidence-not_experimental
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/db_xref="GI:2190540"
/translation="MSINIRDPILYSRVGVLDLPFNRSITLKYTGOREVYNGLDLR
PSQVONKRVLEGEDLNFETLVWVDPDVPSPNHLREYLIHWLVTIDIPATGTTG
NEICYENPSPFAGIHRVFTLFRQLGQTYAAGWQGNFTREFAEIYNGLVAAV
FYNQRESGCCGRRL"
36957..37445
/gene="F5114.4"
join(36957..37065,37294..37445)
/gene="F5114.4"
/codon_start=1
/evidence-not_experimental
/protein_id="AAB60905.1"
/db_xref="GI:2190541"
/translation="MGKSPNIAFMFLPILILFTLSSQLKVESTGKRLAWGFSGTP
IVYPPSRSCGSPAVFTSKWRPRLPGSYIIPASDQSP"
complement(40241..40963)
/gene="F5114.5"
complement(40241..40963)
/gene="F5114.5"
/codon_start=1
/evidence-not_experimental
/protein_id="AAB60906.1"
/db_xref="GI:2190542"
/translation="WCSLEKRDRLFIKLGDGSHRLNPTLLDSLRSTINOIRDPSP
SQSVLITSDSKFPSNGYDLALAESNSLSVMDAKNSLVAADISLPMPIAVTGH
ASAAGCIASHSHVYLMRDRGLFYMSLDIETLVPAPFAVIRGKIGSPARADVML
TAAYVTADVGVKMGIVDSAYGAAETEAALIKLGEIYQRGDGHYGVKMSILLREV
LIHRTGEVSGSVVRSKSL"
complement(41498..42875)
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complement(join(41498..41562,41619..41734,41808..41896,
41981..42127,42220..42267,42316..42564,42795..42875))
/gene="F5114.6"
/note="EST gb|N37484 comes from this gene."
/codon_start=1
/evidence-not_experimental
/protein_id="AAB60907.1"
/db_xref="GI:2190543"
/translation="MAGLKPEAVVQATLSLPDPEVDTVGESEEESEEMAKKESA
SSQKDVALDEMASTAKDANQAKLTLEKHEJQICLSRALAYLASASVWKLITLSS
ILPIGLRSVSMEREELKLVKKEVDILNSVKEGKGDDDEDAKATLAREDSQDRA

gene
CDS
/gene="F5114.7"
/complement(join(42975..43043,43213..43339,43501..43593,43683..43771,43856..44002,44168..44480,44564..44922))
/note="F5114.7"
/note="Similar to Saccharomyces hypothetical protein p9642.2 (gb|U40828)."

/codon_start=1
/evidence=not_experimental
/protein_id="AAB60908.1"
/db_xref="GI:2190544"
/translation="MEGFYRSRLQSPFSNGVIGILEPPLIGLRVLFVPMYSLSLATA
NRPDHRKGEKYSOTKREASPECDKAVGLSLQAKAKAMKEESOKSDISMOWVR
LFLICGRLRALIATSMREDMAKRLHMDDEPSTIOHWLGLKLLMAYRISRLV
KLANGKSLRRERQOLITRTADFLRVPAAVEITVFMELFLVPLKLPNMLPSTFO
DKMKEEALRRRLNARMEYAKFLQDTYKEMAEVQTSRSGELIKTAEEDLVKVR
GVGVSNDLIGFAKLFNDELITLNRSLVNMCKYMGISPECTDAVLYRMLKRLQ
IKKDKLIIKAEVSESLSEAEELRQACRERGMQLQGSVEEMREQLVMDLSLNHVS
LILSR"

gene
CDS
/gene="F5114.8"
/complement(47061..49870)
/gene="F5114.8"
/complement(join(47061..47422,47541..47632,47766..47824,47929..48015,48122..48218,48320..48525,48704..48799,48884..48959,49053..49153,49242..49418,49467..49532,49587..49654,49750..49870))
/gene="F5114.8"
/note="Similar to Zea mays permease 1 (gb|U43034)."

/codon_start=1
/evidence=not_experimental
/protein_id="AAB60909.1"
/db_xref="GI:2190545"
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VGFQHTLSLGLITVLIPSMLEFFFEFFFLURESLILFVAKAVIOTLLEVSILT
TLQSEFGTRLPVIAVASYAIIPITSIITYSTREYITPPEFVETMRISIOALIT
TGEVOYLICILGWNRNIRFLPSLIPATFTGLGHIQGPLIYMMQTSFQOLAR
CSEVGLPGLILIFTOYVLPFLKMKGVAILDGSRCRGMILCIPLVWLFQOLTS
SGVYDHKSHTOTSCRTDRGLITNPMIYIPPCMGSPPTDITDSFAMMAEFTVL
PSTGLIFVARSARVSATPIPSVSGTSCGIVGLNMGITGTCITSTENVGLLA
MTRIGSRVIOISAAPIRFSIFGKRGARFASIPDITMASLVCITVCPCKSSHIH
CSIAFSINICIFETKIKNSIYNASVGLSTYQFCNLMSFNKIFLIGSFFMAISIP
QYFREYNGGMRSDHNSVSTYSIL"

gene
CDS
/gene="F5114.9"
/complement(join(50678..51059,51406..51488,51567..51733,51818..52033,52078..52294,52510..52743))
/gene="F5114.9"
/note="Strong similarity to Arabidopsis zeta-crystallin-like protein (gb|I249268)."

/codon_start=1
/evidence=not_experimental
/protein_id="AAB60917.1"
/db_xref="GI:2190553"
/translation="MGEVSVENKRIKLVNVDGIPETDMEVKGLETTELKAPKSS
CFLVKNLYLSCDPYMRGMRDEHGSYLPVPOKCEVLEPLFGLFIEFEREMC
RCIYALRSCTSPFCDEMIYMLRKLEICILVXKLFIPNDLSIDSVFIYMO
RREGELARVIOSDPTNRKPGDIVSGIITMEESILRSSDNLQRLIOLODDPILSY
LGLLGMAGTAAGNENICCPKKGDSVPFASAGANGOLVGLAKLHGCVYSSASK
OKVEILKNEGLDEAFNYKEADLTKLRPEEGIDITFDVNGSGLMDAALLNMVVR
GRALCGVLSLOSLSTSOGIKNLASYIKRLRLLEQFLSDYLIHIFPOPELVNKRYK
EGKIYVEDISGLDLPALVGLFSGKNIGQVAVAKE"

gene
CDS
/gene="F5114.10"
/complement(join(53168..53386,53596..54114,54461..54916))
/gene="F5114.10"
/note="Strong similarity to Solanum polygalacturonase precursor (gb|U23053)."

/codon_start=1
/product="F5114.10"
/protein_id="AAB60920.1"
/db_xref="GI:2190556"
/translation="MALFLSFVQVPSIVITTIIMSHFGQPDARTSLNVLSEGANPGIV

Query Match 54.4%; Score 466; DB 8; Length 109560;
Best Local Similarity 100.0%; Pred. No. 3.4e-99;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ESAKAPSDAMDAACGEDSVYIVPCKRGLVSGEVRPEGECKREITRLIDDTLIGP
ODYSILGKKRMNMFSPSGVNVAVTVLGGSPGAKSSTLMSCKANGNCEGATTLRFMNSN
NKKIKGVLSLNSOLFPHAIRNCRNKITIEDYRIITAPBESRNTDGIHQSLTDIEVRNAS
IKTGDDCISIGPGTKMLMDGITCGGHGHSISLAKSJEBOGVENVYKNAVEFTD
NGRIKSPHPSHSGFVEYRFLCALIMVNSYPLIDQNCPCGSSCPSOESGKIKINDY
IYSGIMGTSATEIRAIKMDSEKPCVIGIRMOAINLISYGAATSCNTSVSGKOLIVT

QY 26 taaaaataaacactcaatcattcattgattgattataataatataatcgcacacacataata 85
Db 13000 TATAAATATACACTCTTATTCATTCATGATGATTAATATATATCCATCAGACACTATATA 12941
QY 86 agtaaacactctcatttctcccccctcattttataaacactatataatgtaact 145
Db 12940 AGTAAACACTCTCATTTTCTCCCTCTCATTTTATTAACACCTTATATATTTGAAC 12881
QY 146 actaagaacatcacacgcttcgctactcgtatcatataaagtgtataaataaac 205
Db 12880 ACTATAGCATCATCACCCTTCCTTACTCGTATCATTAATAGTTAATTAATTAATAC 12821
QY 206 tatagatgcataaactcattcaatgaagatgcaataatcattggtataaagaagaagca 265
Db 12820 TATAGATGCATTAATATTCATCATCAGATATGCATATCAATTTGTTATTAAGAGAACCA 12761
QY 266 tctaaagtcttctctcccgagccactctccctcgtacaattgtagaagaacgagcga 325
Db 12760 TCTAAAGTCCTCTTCCCTCCGAGCCACTCTCCCTCATCAATTTGTAACAACTCGGCCCA 12701
QY 326 cgggaagaagcagagatgtagatctcagcaactcgcagagtgtagaattctcgagccacc 385
Db 12700 CGGGAAGCCGAGATTGTAGATCTCAGCAACTCGCAGGTTCTGAGGCCACC 12641
QY 386 ctggtgcatacacctgttgcctgcgcaagctgctgcaaaacaatataaacagcagatgaa 445
Db 12640 CTGGTGCATCACCTGTTGCTCGTCCGCAAGCTGCAAAACAATATAACAGCAGATGAA 12581
QY 446 ttctctgagtgaggaacttggaatttcgtataacacaaatctcattgcc 491
Db 12580 TTCTCTGAGTGAGGACTTGGAATTTCTGTAACACACAATCTCATTTGCC 12535

RESULT 8
AF152096/c 2483 bp DNA linear PLN 22-DEC-1999
LOCUS
DEFINITION Arabidopsis thaliana flowering locus T (FT) gene, complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidae; Magnoliophyta; eudicotyledons; core eudicots;
Rhamnales; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS
Kardalinsky, I., Shukla, V.K., Ahn, J.H., Dagenais, N.,
Christensen, S.K., Nguyen, J.T., Chory, T., Harrison, M.J. and
Weigel, D.
TITLE
JOURNAL
MEDLINE
20050959
2 (pages 1 to 2483)
REFERENCE
AUTHORS
Kardalinsky, I. and Weigel, D.
TITLE
JOURNAL
Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
source
location/Qualifiers
1..2483
/organism="Arabidopsis thaliana"
/cultivar="Columbia"

5'UTR mRNA gene CDS

1..63
/gene="FT"
1..2483
/gene="FT"
join(64..264,1080..1141,1855..1895,2020..2483)
/product="flowering locus T"
/gene="FT"
/function="induces flowering"
/note="similar to hippocampal cholinergic neurostimulating peptide (HCNP) precursor, phosphatidylethanolamine binding protein (PEBP) and Raf kinase inhibitor protein (RKIP); corresponds to Arabidopsis thaliana BAC F5114 sequence presented in Genbank Accession Number AC001229"

/codon_start=1
/product="flowering locus T"
/protein_id="AA03936.1"
/db_xref="GI:6117978"
/db_xref="GI:6117978"
/translation="MSINRDPILVRSVGVLDPPRSLIKVYGVREYNGDLR PSYONKPRVIEGDDRNFTYLVMDPPVPSBNPRLREHLHYDIPATTTTCG NEVCYENPSPSGIHRVFLFRQLGRQTVIAGVMDNTRFETIYDLGLPAAY FYNCQRESGGGRRL"
2483

polya_site
/gene="FT"
BASE COUNT 762 a 391 c 407 g 923 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 465; DB 8; Length 2483;
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 ataatataaacattcatctatgagatataataataatcgcacacacatatataa 86
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2483 ATAAATATAACACTTCATTTGATGATATATATATATATATATATATATAT 2424

87 gtaaaacacatcatcttcccccctcattttatataacacattatataa 146
|||||
2423 GTAATAACACTTCATTTGATGATATATATATATATATATATATATAT 2364

147 ctatagacatcaacacgctcgttactcgtatcataaaatggttataataa 206
|||||
2363 CTATAGCATATACACCGCTGCTGCTGCTATCAATAAATGTTATTAATAA 2304

207 atagatgataaataatctatcagagatgataatataatggttataaaagaag 266
|||||
2303 ATAGATGATATAAATCTCATACAGATATCAATTCATTTGATTAAGAAG 2244

267 ctaaaagcttctcccgagacacatccctcgtacaattgtagaanaactgcgc 326
|||||
2243 CTAAGAAGCTTCTCTCCGCGACACCTCCCTCGACATTTGAGAAACCTGCG 2184

327 gggaagcgcgagatgtagatcctaagaactcgcgagtggtgaagctcgcgc 386
|||||
2183 GGGAAAGCGCGAGATGTGATCTCAGCAAACTCGCGAGTGTGAAGTCTGCG 2124

387 tgggtgatacactgttcccgcaagctgtcgaagaacttaaacagagaagtgat 446
|||||
2123 TGGTGCATACACTGTTTCCCTGCGCAAGCTGTGGAACAATTAACACGACG 2064

447 tccgcaatgggaactgtgatttcgtaacacaaatcattgac 491
|||||
2063 TCCTGCACTGGGACTTGGATTTTCTTAACACAACTCATTGCC 2019

RESULT 9
AB027506/c
LOCUS
DEFINITION Arabidopsis thaliana t5f (TWIN SISTER OF FT) mRNA, complete cds.

AB027506
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
CDS
gene
CDS

AB027506
AB027506.1 GI:4903015
t5f.
Arabidopsis thaliana (strain: Columbia) cDNA to mRNA.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (sites)
Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.
A pair of related genes with antagonistic roles in mediating flowering signals
Science 286 (5446), 1960-1962 (1999)
2 (bases 1 to 799)
Araki, T. and Kobayashi, Y.
Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail: taraquiegr.bot.kyoto-u.ac.jp, Tel: 81-75-753-4136, Fax: 81-75-753-4141)
Location/Qualifiers
1..799
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="4"
/map="next to LSD1 locus"
32..559
/gene="t5f"
32..559
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/standard_name="TWIN SISTER OF FT"
/note="extensive homology with FT; similar to mammalian phosphatidylethanolamine binding protein (PEBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor"
/codon_start=1
/product="t5f"
/protein_id="BA077840.1"
/db_xref="GI:4903016"
/translation="MSLSRDPILVRSVGVLDPPRSLIKVYGVREYNGDLR PSYONKPRVIEGDDRNFTYLVMDPPVPSBNPRLREHLHYDIPATTTTCG NEVCYENPSPSGIHRVFLFRQLGRQTVIAGVMDNTRFETIYDLGLPAAY FYNCQRESGGGRRL"
772..777
polya_signal
BASE COUNT 222 a 152 c 182 g 243 t
ORIGIN

Query Match
Best Local Similarity 76.6%; Score 389.8; DB 8; Length 799;
Matches 505; Conservative 0; Mismatches 147; Indels 7; Gaps 2;

157 catcacgctgctactcgtatcataaataatggttataataaata----ctagatg 213
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676 CATCATTTTCTTACCTGCTGATTAATTCCTTATTAATTCATTAATTCATTA 617

214 cataaactcatcagagatgataatcaatggttataaagaagaag----ccatcta 269
|||||
616 CTTCAATTAAAGGAATATTAATGATTAATTAATTAATTAATTAATTAATTA 557

270 aagcttctccctccgacacatccctcgtacaattgtagaanaactgcgcgaag 329
|||||
556 CGTTCTTCTCCCGACAGCATTTCTCCCTGCGAGTTGAAGTGAAGAGCGACAG 497

330 aagcgcgagatgtagatcctaagaactcgcgagtggtgaagctcgcgcaccc 389
|||||
496 AAGACCAAGATGTGATCTCAGCAAACTCAGATGTGTAAGCTGTGCGCCACCC 437

390 tgcatacactgttcccgcaagctgtcgaagaacttaaacagagaagatgaatcc 449
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[illegible]

FEATURES	source	CC FT	Key source	Location/Qualifiers Location/Qualifiers 1. .528 /organism="Arabidopsis" /db_xref="taxon:3701"	Location/Qualifiers 1.528 /organism='Arabidopsis'
BASE COUNT	122 a	117 c	142 g	147 t	
ORIGIN					
Query Match	43.7%	Score 374.4;	DB 6;	Length 528;	
Best Local Similarity	81.8%;	Pred. No. 1.3e-77;			
Matches 432;	Conservative	0;	Mismatches 96;	Indels 0;	Gaps 0;
Oy	267	ctaaagcttcttctctccgcagccactctccctcgacaattgtgtgaaaaacttgccac	326		
Db	528	ctacgctttcttctcccccacacgcatctctccctcgaggtgaaggaagccac	469		
Oy	327	gggaagcgcgagatgtgtatctcagcaactcgcgagtggttgaagttctgagccacc	386		
Db	468	aggaagaccagattgtgtatctcagcaactcagcagatgtttgaactgttgccgccacc	409		
Oy	387	tgtgtacatacctgttgcctgcgaagctgttcgaacaatabaaacagcaacgaatgaat	446		
Db	408	cggtcgcatmaacccgtttctctccgagttgccggaacatcacaacacaaatgacatgaat	349		
Oy	447	tcctcagtgagacttgatgttctgttaacacacaatctcatgtccaaagtgttcagat	506		
Db	348	tcccgaggggggacgtgactctctgtacacacacacctcatgttgcgaagggcattttccagt	289		
Oy	507	tgtagcaggaatcacgtcaccaacaaatgtgagatattctcggaggtgaggtgtctag	566		
Db	288	ggtggcaggtatattcagtcaccacacacacagtgagatattctggtgaggggtcttgg	229		
Oy	567	acttgaaacatctgatactcaacataccaagataagaagtctcctgagctcttccacc	626		
Db	228	actgcgacatcagatccacacatcaccagaggtgagaaatttctgaaagtctctctcc	169		
Oy	627	aatcacaactcttggtctgttctgaaccttgaaagggccttgaatccaaagcattagac	686		
Db	168	aattctccactattgtgtgtgttcagaaactttgaaagggccttgaatccaaagcattagac	109		
Oy	687	ctctcttggccataagtaaacctttagagtgtatgtatctatctaaacgataagaagctc	746		
Db	108	ctctcttggccataagtaaacctttagagtgtatgtatctatctaaacgataagaagctc	746		
Oy	747	tccaaacactctgtctactataaaggaggtctcttatctatctataagacat	794		
Db	48	tccaaacactctgtctactataaaggaggtctcttatctatctataagacat	1		
RESULT 12	AB027456/c	745 bp	mRNA	Linear	PLN 26-FEB-2000
LOCUS	AB027456				
DEFINITION	Citrus unshiu ClfT mRNA, complete cds.				
ACCESSION	AB027456				
VERSION	AB027456.1	GI:4903138			
KEYWORDS	ClfT.				
SOURCE	Citrus unshiu (strain: Miyagawa-wase satsuma mandarin) developing stage juice sac and pulp segment cDNA to mRNA.				
ORGANISM	Citrus unshiu				
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Sapindales; Rutaceae; Citrus.				
AUTHORS	Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Arai, T.				
TITLE	A pair of related genes with antagonistic roles in mediating flowering signals				
JOURNAL	Science 286 (5446), 1960-1962 (1999)				
MEDLINE	20050958				
REFERENCE	2 (bases 1 to 745)				

AUTHORS	Omura, M., Kobayashi, Y. and Areaki, T.
TITLE	Direct Submission
JOURNAL	Submitted (17-May-1999) Mitsuo Omura, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu, Shizuoka, Shizuoka 424-0292, Japan (E-mail:om9330@okt.affrc.go.jp, Tel:81-543-69-7108, Fax:81-543-69-2115)
FEATURES	Location/Qualifiers 1..745
SOURCE	/organism="Citrus unshiu" /strain="Miyagawa-vase satsuma mandarin" /db_xref="taxon:55188" /dev_stage="developing stage juice sac and pulp segment" Accession Number C24153"
gene	96..629 /gene="ClFt"
CDS	96..629 /gene="ClFt" /note="extensive homology to FT (FLOWERING LOCUS T, AB027504) and TSF (TWIN SISTER OF FT, AB027506) genes of Arabidopsis thaliana; similar to mammalian phosphatidylinositol binding protein (PBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor /codon_start=1 /protein_id="BAA77836.1" /db_xref="GI:4903139" /translation="MSRSRDLPLGVVGDVLNDFRTIPMRITYSNKDVNGRELK PSEVLNCPRAIEGDDLRFTLYLWVPDAPSPDELRXLMLVDIPIATGASFG OEIVLNESPRPTMGIDHREVFVLERLQROIVYAPGRMNSTNDFAELYNLGPAVAY YFNCRSGSSGSRRVVR"
BASE COUNT	195 a 150 c 180 g 220 t
ORIGIN	
Query Match	33.8% Score 289.6; DB: 8; Length 745;
Best Local Similarity	72.3% Pred. No. 9.8e-58;
Matches 376; Conservative	0; Mismatches 144; Indels 0; Gaps 0;
Oy	277 ctctccgcgacgaactctcctctgtacaatttgtagaacctcgccacggaaaggccg 336
Dd	613 CTTCGCCGGAGATCCGCCTCCTCGACATTGAAGTAGACAGCGGCGCACCGAGGTCCC 554
Oy	337 agattgtagatctcaagaacctcgagtglttgaagtcttcgcccaccctggtgcatac 396
Dd	553 AGATTGTAAAGCTCAGCAAAATCCCTCGTGCTGAAGTTCTACGCCACCGTGTCATAA 494
Oy	397 actgttttcgcgcgaagtgtgcgaacaataaacaagacagcatgatgaattcctgcagtg 456
Dd	493 ACAGCTGCTGCCATCCAGAATGTGCGGAAACAACAAGAACAAACGTGTGAATCCCATCGTT 434
Oy	457 ggaacttgatttcgttaaacacaaatctcatgtccaaaagttgttccaagttgttagcaagg 516
Dd	433 GGCCCTTAGGGCTTTCATTAAGTTACAAATCTCTTGCGCCAAAGCTGGGCCCTGTGGTGGGA 374
Oy	517 atatacagtcaccaacaatgagatatcttcggaggtgtaagggttgcatacgaactggagaca 576
Dd	373 ATATAGTCACCACCAACCATGCAAAATACACCTCCATAGCGCTGGGGTGCATTGGGCTTGGTGA 314
Oy	577 tcgtgaatcacacaataacaaagtataagaagtcttcctgaagtcctctccacaacatccaaact 636
Dd	313 TCAGGATCAACCATTTACCAAAGTATAAAATGTCTTAAGATCATACACCAACTTTCAGGCC 254
Oy	637 cttagtctggttttgaaactctggaaggccttatagatccaagcatatagtcactctctcttg 696
Dd	253 CTAGGCTGGTTTCAGAACTTCAGAAAGTTTGAGCTACGCGCCATTATTAATCACTCTTGTTT 194
Oy	697 caataagaacacttagtgatgcatactataacaagcataaagaacgtcccaacaact 756
Dd	193 GAATAGGTAATTCCTCATTTGGAAATGTTCTTTTAAATTTGTCAAGAACATCCAAACAAGC 134
Oy	757 ctgctaactaagaaggctctctataattatataacatct 796

Db	133	C6GCCACATPATAAGAGATCTCTCCTCCCTGCTAGACATAT	94
<hr/>			
RESULT	13		
LOCUS	ABO52943	847 bp	mRNA linear PLN 21-JUN-2001
DEFINITION	Oryza sativa Hd3a mRNA, complete cds, cultivar:Kasalath.		
ACCESSION	ABO52943		
VERSION	ABO52943.1	GI:14517621	
KEYWORDS			
SOURCE			
ORGANISM	Oryza sativa (cultivar:Kasalath) cDNA to mRNA.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.		
AUTHORS	Kojima,S., Monna,L., Fuse,T., Sasaki,T. and Yano,M.		
TITLE	Hd3a, a quantitative trait locus, involves in the promotion of flowering in rice		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 847)		
AUTHORS	Yano,M. and Kojima,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-DEC-2000) Masahiro Yano, National Institute of Agrobiological Resources, Department of Molecular Genetics; 2-1-2 Kamohara, Tsukuba, Ibaraki 305-8607, Japan (E-mail:myanoeabr.affrc.go.jp, Tel:81-298-38-7443, Fax:81-298-38-7468)		
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AUTHORS	1 (sites)		
TITLE	Kojima,S., Monna,L., Fuse,T., Sasaki,T. and Yano,M.		
	Hd3a, a quantitative trait locus, involves in the promotion of flowering in rice		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 847)		
AUTHORS	Yano,M. and Kojima,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-DEC-2000) Masahiro Yano, National Institute of Agricultural Resources, Department of Molecular Genetics, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan		
	(E-mail:myanob@affrc.go.jp, tel:81-298-38-7443, Fax:81-298-38-7468)		
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DEFINITION Oryza sativa RFT1 mRNA for FT-like protein, complete cds.
ACCESSION AB062676
VERSION AB062676.1 GI:17221651
KEYWORDS
SOURCE Oryza sativa (cultivar:Nipponbare) cDNA to mRNA.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Kojima,S., Lisa,M., Takahashi,Y., Sasaki,T. and Yano,M.
TITLE The photoperiod sensitivity gene Hd3a promotes flowering in rice
JOURNAL unpublished
REFERENCE 2 (bases 1 to 866)
AUTHORS Yano,M. and Kojima,S.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-2001) Masahiro Yano, National Institute of
Agricultural Sciences, Department of Molecular Genetics; 2-1-2
Kannonnai, Tsukuba, Ibaraki 305-8602, Japan
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Fax:81-298-38-7468)

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